

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 175267

TO: Sarvamangala Devi

Location: REM-3B07/3C18
Art Unit: 1645

Friday, January 0 2006

Case Serial Number: 09/445517

From: Kristine

**Location: Biotech-Chem Library** 

**REM-1B69** 

Phone: (571)272-4161

Kristine.Hensle@uspto.gov

#### Search Notes

Examiner Devi,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle Librarian STIC Biotech/Chem Library (571)272-4161



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#### STIC-Biotech/ChemLib

175267

From:

Devi, Sarvamangala

Sent:

Thursday, December 29, 2005 9:19 AM

To:

STIC-Biotech/ChemLib

Subject:

09/445,517

In application 09/445,517, please perform a sequence search for SEQ ID NO: 14 in pending and commercial databses. Please provide me with a paper copy of first 50 hits.

Thanx.

S. DEVI, Ph.D. Primary Examiner AU 1645 Rems - 3C18

RECEIVED

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#\_\_\_\_\_\_AA#:

S/L:\_\_\_\_Oligomer:\_\_\_\_

Encode/Trans!\_\_\_\_

Structure #:\_\_\_\_Text:\_\_\_

Inventor:\_\_\_\_ Litigation:\_\_\_\_

Vendors and cost where applicable STN:
DIALOG:
QUESTEL/ORBIT:
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SEQUENCE SYSTEM:
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Other (Specify):

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US-10-516-768-10

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Publication No. US20050256302A1
GENERAL INFORMATION:
APPLICANT: MINAMINO, NAOTO
TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
FILE REPRENCE: 62273(71526)
CURRENT APPLICATION NUMBER: US/10/516,768
CURRENT APPLICATION NUMBER: US/10/516,768
CURRENT APPLICATION NUMBER: PCT/JP03/06641
PRIOR FILING DATE: 2003-05-28
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 52
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                   US-10-516-768-26
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APPLICANT: Ancesin, John B.
APPLICANT: Ancesin, John B.
APPLICANT: Elimova, Elena
APPLICANT: Elimova, Elena
APPLICANT: Elimova, Elena
APPLICANT: Elimova, Robert
TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
TITLE OF INVENTION: Identification and Use
FILE REFERENCE: PTQ-0066
CURRENT APPLICATION NUMBER: US/11/098,674
CURRENT FILING DATE: 2005-04-04
PRIOR PLILING DATE: 2004-04-02
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US-200-516'-5'68-2

Publication No. US20050256302A1

GERERAL INFORMATION:

APPLICANT: MINAMINO. NACTO

APPLICANT: MATAFUCHI, TAKESHI

ITILE OF INVENTION: NOVBL PRETIDES HAVING CAMP PRODUCING ACTIVITY

FILE REFERENCE: 6223(71526)

CURRENT FILING DATE: 2004-12-03

PRIOR PILING DATE: 2004-12-03

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-28

PRIOR PILING DATE: 2002-06-3

SOFTWARE: Patentin Ver. 3.3

SQOTWARE: Patentin Ver. 3.3

SQOTWARE: PRIOR TILING DATE: COURTH OF THE INFORMATION: C-term amidated

CHER INFORMATION: C-term amidated
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Pred. No. 5.3e-05;
0; Mismatches 2; Indels
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73.4%; Score 102; DB 6;
Best Local Similarity 62.9%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 13.
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SOFWWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 30
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SOFTWARE: PatentIn Ver. 3.3
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Matches 12; Conservative
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US-11-098-674-13
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-10-516-768-8
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TITLE OP INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OP INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-03-3
SOFTWARE: PATENTIAL OF THE STANDARD SOFTWARE: PATENTIAL OF THE STANDARD SOFTWARE: PATENTIAL OF THE STANDARD SOFTWARE: DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PATENTIAL OF THE STANDARD SOFTWARE SOT DATE: 2004-02-06
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                                  Query Match
30.9%; Score 43; DB 6; Length 37;
Best Local Similarity 34.3%; Pred. No. 0.035;
Matches 12; Conservative 1; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%; Score 43; DB 6; Length 37; 34.3%; Pred. No. 0.035; tive 1; Mismatches 22; Indels
                                                                                                                       3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                             3 NTATCVTHRLAGLLSRSGGMVKSNFVPTDVGSEAF 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: C-term amidated US-10-516-768-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Helicobacter pylori J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 34.3 ies 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-11-052-554A-103
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US-10-516-768-23
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Gaps
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; Publication No. US20050256302A1
; GENERAL INFORMATION;
APPLICANT: MINAMINO, NAOTO
; APPLICANT: MINAMINO, NAOTO
; APPLICANT: KATAPUCHI, TAKESHI
TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
; FILE REPERENCE: 62273(15.26)
; CURRENT APPLICATION NUMBER: US/10/516,768
; CURRENT FILING DATE: 2004-12-03
; PRIOR FILING DATE: 2003-06-28
PRIOR FILING DATE: 2003-06-28
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.6%; Score 37; DB 35.5%; Pred. No. 1.9; tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 24, Application US/10516768
; Publication No. US20050256302A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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6 TXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37

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Query Match
Best Local Similarity
                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Sus sp.
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US-10-516-768-2
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US-10-516-768-4
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                                                                                                                                                                                    LENGTH: 38
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; Sequence 30, Application US/10516768
; Publication No. US20050256302A1
; GENERAL INFORMATION:
APPLICANT: HANAMINO, NAOTO
; APPLICANT: KATAFUCHI, TAKESHI
; TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
ITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
FILE REFERENCE: 62273(71526)
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/JP03/06641
; PRIOR APPLICATION NUMBER: PCT/JP03/06641
; PRIOR APPLICATION NUMBER: 2003-06-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver: 3.3
; SEQ ID NO 30
LENGTH: 37
          APPLICANT: MARGENIA MACION; APPLICANT: KATAFUCHI, TARESHI
TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
FILE REPERENCE: 62273 (71256)
CURRENT APPLICATION NUMBER: US/10/516,768
CURRENT PILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: PCT/JP03/06641
PRIOR APPLICATION NUMBER: PCT/JP03/06641
PRIOR PILING DATE: 2003-05-28
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PALENTIN VEY: 3.3
SEQ ID NO 24
LENGTH: 37
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Publication No. US20050256302A1
Publication No. US20050256302A1
APPLICANT: MINAMINO, NAOTO
APPLICANT: KATAFUCHI, TAKESHI
FITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
FILE REFERENCE: 62273 (71526)
CURRENT APPLICATION NUMBER: US/10/516,768
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25.9%; Score 36; DB 6; Length 37;
Best Local Similarity 31.4%; Pred. No. 0.8;
Matchés 11; Conservative 2; Mismatches 22; Indels
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CTHER INFORMATION: C-term amidated
US-10-516-768-30
                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: C-term amidated US-10-516-768-24
APPLICANT: MINAMINO, NAOTO
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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US-10-516-768-1
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Sequence 2, Application US/10516768

Publication No. US20050256302A1

GENERAL INFORMATION.

APPLICANT: MINAMINO, NAOTO

APPLICANT: MINAMINO, NAOTO

APPLICANT: MATAFUCHI, TAKESHI

TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY

FILE REPERENCE: 6273 (11526)

CURRENT APPLICATION NUMBER: US/10/516,768

CURRENT FILING DATE: 2004-12-03

FRIOR APPLICATION NUMBER: US/10/03/06641

PRIOR FILING DATE: 2003-05-28

PRIOR FILING DATE: 2003-06-04

NUMBER OF SEQ ID NOS: 52

SEQ ID NO 2

SEQ ID NO 2
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APPLICANT: MINGMINO, NAOTO
APPLICANT: KATARUCHI, TAKESHI
TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
FILE REFERENCE: 62273/11526)
CURRENT TILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: PCT/JP03/06641
PRIOR APPLICATION NUMBER: PCT/JP03/06641
PRIOR FILING DATE: 2003-05-28
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PALCHIN Ver. 3.3
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0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION WUMBER: PCT/JP03/06641
PRIOR FILING DATE: 2003-05-28
PRIOR FILING DATE: 2003-05-28
PRIOR FILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PALENTIN VET. 3.3
                                                                                                                                                                                                                                                              FEATURE:
; OTHER INFORMATION: C-term may be amidated US-10-516-768-1
                                                                                                                                                                                                                                                                                                                                                     Query Match 25.9%; Score 36; Best Local Similarity 31.4%; Pred. No. Matches 11; Conservative 2; Mismatcl
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Kroger, Burkhard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FOMPELUS, MAIXANG
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gargor
TITLE OF INVENTION: CORYNEBEACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-03-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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                                                                                                                                                         25.9%; Score 36; DB 6; Length 126; 31.4%; Pred. No. 3; tive 2; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                             83 NTATCMTHRLVGLLSRSGSMVRSNLLPTKMGFKVF 117
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US-11-055-822-228
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Sequence 716, Application US/11055822
; Publication No. US220520260707A1
; GENERAL INFORMATION:
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Publication No. US20050260707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No. US2005026070:
GENERAL INPORMATION:
APPLICANT: Pompejus, Markus
                                                                                                                                                                                                                  11, Conservative
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Best Local Similarity
                                                                                                                                                                                   Best Local Similarity Matches 11; Conserva
                                                 ; TYPE: PRT
; ORGANISM: Sus sp.
US-10-516-768-4
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US-11-055-822-228
; SEQ ID NO 4
; LENGTH: 126
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ORGANISM:
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APPLICANT: Zelder. Obkar

APPLICANT: Zelder. Obkar

APPLICANT: Zelder. Obkar

TITLE GO INVERTION: CORVERACTERING GUITAMICHO GENES ENCODING

TOTAL SELDER PRINCE APPLICATION MUMBER: 09/14/031

PRIOR FILING DATE: 1099-00-6-23

PRIOR FILING DATE: 1099-00-6-23

PRIOR FILING DATE: 1099-00-6-23

PRIOR FILING DATE: 1099-00-6-23

PRIOR FILING DATE: 1099-00-10

PRIOR PRIOR FILING DATE: 1099-00-10

PRIOR PRIOR FILING DATE: 1099-00-10

PRIOR PRIOR PRIOR DATE: 1099-00-10

PRIOR PRIOR PRIOR DATE: 1099-00-10

PRIOR PRIOR PRIOR DATE: 1099-00-10

PRIOR FILING DATE: 109
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RESULT 18
US-11-055-822-714
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PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR PELICATION NUMBER: DE 19931418.7
PRIOR PILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR PELICATION NUMBER: DE 19931420.9
PRIOR PELING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
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APPLICANT: Bailey, Richard B.
APPLICANT: Bailey, Richard B.
APPLICANT: Bonequist, Paul
APPLICANT: Doten, Reed
APPLICANT: Doten, Reed
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: Walbridge, Michael J.
APPLICANT: JONED PRODUCTION
CURRENT APPLICATION NUMBER: US 60/475,000
PRIOR PRILNG DATE: 2003-05-30
PRIOR PILING DATE: 2003-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 7; Length 600;
Pred. No. 16;
1; Mismatches 3; Indels
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; ORGANISM: Coryne-bacterium glutamicum
US-10-858-730-224
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 224, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
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; Sequence 226, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.9%;
60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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LENGTH: 600
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Sequence 2, Application US/11168476
Publication No. US20050266535A1
GENERAL INFORMATION:
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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        411 PALPTTTIGS 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
PRIOR APPLICATION WUBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-07-08
PRIOR PLILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 714
LENGTH: 745
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NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL LINGUATES DE LA PARKUS
APPLICANT: ROGET, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Chartwig
APPLICANT: Schroder, Chartwig
APPLICANT: Controler, Hartwig
APPLICANT: Controler, Gregor
TITLE OF INVENTION: CORYMBEATERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYMBEATERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYMBER: US/11/055,822
CURRENT FILING DATE: 2005-05-23
FILOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-714
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US-11-055-822-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-055-822-756
; Sequence 756, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
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Best Local Similarity 60.0
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Best Local Similarity 60.0
Matches 6; Conservative
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LENGTH: 745
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25 PXLPXTXVGS 34

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APPLICANT: MOGLALLA BELLIANA
APPLICANT: PEFFEREL, BELLIANA
APPLICANT: HUTHMACHER, KLAUS
APPLICANT: RUGCKERT, CHRISTIAN
APPLICANT: RUGCKERT, CHRISTIAN
APPLICANT: RUGCKERT, CHRISTIAN
APPLICANT: PUEHLER, ALFRED
APPLICANT: BINDER, MICHAEL
APPLICANT: BINDER, MICHAEL
APPLICANT: BINDER, MICHAEL
APPLICANT: THERBACH, GEORG
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METE GENE
FILE REPREMENCE: 211710USGX
CURRENT APPLICATION NUMBER: US/09/919,835
PRIOR APPLICATION NUMBER: US/09/919,835
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VETEIN VETEIN 3.1
SEQ ID NO 2
LENGTH: 745
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; Publication No. US2006025302A1
; GENERAL INFORMATION:
; APPLICANT: MINAMINO, NACTO
; APPLICANT: MINAMINO, NACTO
; APPLICANT: MINAMINO, NACTO
; PILE REFERENCE: 62273(1256)
; CURRENT PEPLICATION NUMBER: US/10/516,768
; CURRENT PEPLICATION NUMBER: US/10/516,768
; CURRENT PEPLICATION NUMBER: PCT/JP03/06641
; PRIOR APPLICATION NUMBER: PCT/JP03/06641
; PRIOR PILING DATE: 2003-05-28
; PRIOR PILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 33
; LENGTH: 23
; TYPE: PRI
; PRATIRE:
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LOCATION: (2)
OTHER INFORMATION: Variable amino acid
FEATURE:
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; ORGANISM: Corynebacterium glutamicum
US-11-168-476-2
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24 NVGPGLPGTYI 34
 225 LPLAVVGSNT 234
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Best Local Similarity
                                                                       US-10-454-437-38
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                                                                                                                                                                                                                                                       RESULT 22
US-10-793-626-2812
Squence 2812, Application US/10793626
; Squence 2812, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KINMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT PILING DATE: 1999-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PALCHIN Ver. 2.1
; SEQ ID NO 2812
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                                                                                        DB 6; Length 23; 0.75;
                                                                                                                             5; Indels
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US-10-878-556A-78
US-10-878-556A-78
Sequence 78, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REPRENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILIG DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SEQ ID NO 78
LENGTH: 418
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw_hum/sep7_human
DATABASE BYNTY DATE: 1997-11-01
US-10-878-556A-78
                                                                                        Score 35; DB
Pred. No. 0.75
0; Mismatches
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: Variable amino acid
US-10-516-768-33
                                                                                          25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                3 NTATXATORLXNFL 16
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162 PDLPTTTIGS 171
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                                                                           Query Match
Best Local Similarity
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Best Local Similarity
Matches 7; Conserva
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27 LPXTXVGSNT 36

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RESULT 24

US-10-45-47-18

US-10-45-47-18

Publication No. US-005027711AA1

Publication No. US-005027711AA1

APPLICAT: Populate HARAC

ITTLE OF INVESTION: CONFESSED HARAC

APPLICATION: POPULATION: CONFESSED HARAC

TITLE OF INVESTION: CONFESSED HARAC

CURRENT APPLICATION NUMBER: DE 1931125 6

PRIOR APPLICATION NUMBER:
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Gaps
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Publication No. US20050251873A1
GENERAL INFORMATION:
APPLICANT: PENNINGER, JOSEPH M.
APPLICANT: CRACKOWER, MICHAEL A.
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
                                                                                                                                                                                                                                                                                                                                                                                                    ö
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GUREAKLI INCORATION:
GREEKLI INCORATION:
APPLICANT: Balley, Faul
APPLICANT: Dingquist, Paul
APPLICANT: Driggers, Edward M.
APPLICANT: Driggers, Edward M.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Leary, Jessica
APPLICANT: O'Toole, George
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Michael J.
APPLICANT: Walbridge, Michael J.
APPLICANT: Walber: US 60/475,000
PRIOR FILING DATE: 2003-05-30
PRIOR PRIOR FILING DATE: 2004-06-01
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 772
                                                                                                                                                                                                                                                                                                                                                     Length 771;
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APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NOS: 9218
SEQ ID NO 5562
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Score 34; DB 6; 60.0%; Pred. No. 52; tive 1; Mismatches
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Pred. No. 52;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 77, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces coelicolor
US-10-858-730-77
                                                                                                                                                                                                                                                                               ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5562
                                                                                                                                                                                                                                                                                                                                                     24.5%;
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439 PPLPTTTIGS 448
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Driggers, Revin T.
APPLICANT: Madden, Kevin T.
APPLICANT: O'Toole, George
APPLICANT: O'Toole, George
APPLICANT: Trucheart, Joshua
APPLICANT: Trucheart, Joshua
APPLICANT: Worgey, Peter S.
TITLE OF INVENTION: PRODUCTION
TITLE OF INVENTION: PRODUCTION
FILE REPERRECE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR PILING DATE: 2003-05-30
PRIOR PILING DATE: 2003-05-30
PRIOR PILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                           24.5%; Score 34; DB 6; Length 759; 60.0%; Pred. No. 51; tive 1; Mismatches 3; Indels
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Pred. No. 51;
1; Mismatches 3; Indels
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
FRIOR APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR PILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PESSEQ for Windows Version 4.0
SOFTWARE: 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5562, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                         ) ORGANISM: Mycobacterium tuberculosis
US-10-858-730-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mycobacterium leprae
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Driggers, Edward M.
Madden, Kevin T.
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity
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US-10-467-657-5562
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LENGTH: 760
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RESULT 32
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Sequence 533, Application US/10995561

Sequence 533, Application US/10995561

Sequence 533, Application US/1099561

Sequence 533, Application US/1099561

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1559

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 533

LENGTH: 271
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TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
FILE REPERENCE: SONN:064US
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT FILING DATE: 2004-12-17
FRIOR PEDILGATION NUMBER: PCT/CA03/00882
FRIOR APPLICATION NUMBER: US 60/389,709
FRIOR APPLICATION NUMBER: US 60/389,709
FRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Version 3.1
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 242, Application US/10510386
| Publication No. US20050244922A1
| GENERAL INFORMATION:
| APPLICANT: Andersen, Jens Tonne
| APPLICANT: Clausen, Ib Groth
| APPLICANT: Clausen, Ib Groth
| APPLICANT: Glausen, Ib Groth
| APPLICANT: Glausen, Ib Groth
| APPLICANT: Glausen, Ib Groth
| APPLICANT: Rasmussen, Michael Dolberg
| TITLE OF INVENTION: Improved Bacillus Host Cell
| FILE REFERENCE: 10294.204-US
| CURRENT APPLICATION NUMBER: US/10/510,386
| CURRENT APPLICATION NUMBER: US/10/510,386
| UNDMERS OF SEQ ID NOS: 248
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 242
| LENGTH: 247
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Pred. No. 2
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Best Local Similarity 39.1%; Pred. No. !
Matches 9; Conservative 3; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative 3
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US-10-510-386-242
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APPLICANT: Schroder, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: MATABOLIC PATHWAY PROTEINS
FILE REFERENCE: BG1-121CPCVN
CURRENT PALLICATION NUMBER: US/11/055,822
CURRENT PILLOR DATE: 2005-02-11
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Pred. No. 32;
5; Mismatches 16; Indels
                                                                        Length 271;
                                                                                                                     Indels
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APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Warkus
APPLICANT: HUMBELIN, Markus
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: WELSEW, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT PILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 88
LENGTH: 325
                                                                      DB 6;
26;
                                                                                                                     Mismatches
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PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR PLING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR PLILING DATE: 1999-07-01
PRIOR PLILING DATE: 1999-07-08
                                                                        Score 33;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                   ; Sequence 88, Application US/11129143; Publication No. US20050266518A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Enterococcus faecium US-11-129-143-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
23.7%;
Best Local Similarity 25.0%;
Matches 7; Conservative 5
                                                                   Query Match 23.7%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                                                                                                                     25 PXLPXTXVGSNT 36
; ORGANISM: Homo sapiens
US-10-995-561-533
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APPLICATION NUMBER: DE 19931418.7

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APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FOUTAN Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAN Vega
APPLICANT: MONACI Elisabetta
ITILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT APPLICATION NUMBER: GB-0103424.8
FRIOR RELING DATE: 2003-08-11
FRIOR RELING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOCTWARE: Seqwing9, version 1.04
SEQ ID NO 7592
                                                                      Sequence 7592, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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267 NTAPQSLERILNF 279
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267 NTAPQSLERILNF 279
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Best Local Similarity
Matches 6; Conserv
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US-11-055-822-290
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APPLICANT: Schroder, Hartwig
APPLICANT: Gelder, Obskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BG1-121CPCM
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT APPLICATION NUMBER: G00-02-11
PRIOR PELING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PELING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: G0/148,613
PRIOR APPLICATION NUMBER: G0/148,613
PRIOR PELING DATE: 1999-06-12
PRIOR PELING DATE: 1999-00-01
PRIOR PELING DATE: 1999-00-01
PRIOR PELING DATE: 1999-07-08
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        PRIOR APPLICATION NUMBER: DE 1991420.9

PRIOR APPLICATION NUMBER: DE 19931420.9

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1158

SEQ ID NO 302

LENGTH: 382
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                                                                                                                                                                                                                                                                                                                       13.7%; Score 33; DB 7; Length 382; Sonsity 53.8%; Pred. No. 38; Conservative 1; Mismatches
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Pred. No. 38;
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FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931419.5
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                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 344, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            Sequence 8366, Application US/10467657

Sequence 8366, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: FINION SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: FONTANA Maria Rita

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

ITILE OF INVENTION GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT PILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

SPRIOR APPLICATION NUMBER: GB-0103424.8

SOFTWARE: Sequing) version 1.04

SEQ ID NO 8366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 6; Length 408;
Pred. No. 41;
                                                                                  Length 408;
                                                                                                                                4; Indels
                                                                                Score 33; DB 6;
Pred. No. 41;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 290, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8366
TYPE: PRT ORGANISM: Neisseria gonorrhoeae
                                                                                  23.7%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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; TYPE: PRT
; ORGANISM: Petunia hybrida
US-11-054-385-12
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US-11-124-368A-300
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APPLICANT:
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APPLICANT:
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APPLICANT: Eurkhard
APPLICANT: Schooder Hartwig
APPLICANT: Schooder Hartwig
APPLICANT: Schooder Hartwig
APPLICANT: Schooder Hartwig
APPLICANT: Estect, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEAGCTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: MURBER: 2005-02-11
CURRENT APPLICATION NUMBER: 09/606,740
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-25
FRIOR PELING DATE: 1999-06-25
FRIOR APPLICATION NUMBER: 60/148,613
FRIOR APPLICATION NUMBER: DE 19931418.7
FRIOR PELING DATE: 1999-07-08
FRIOR APPLICATION NUMBER: DE 19931419.5
FRIOR PELING DATE: 1999-07-08
FRIOR APPLICATION NUMBER: DE 19931420.9
FRIOR FILING DATE: 1999-07-08
FRIOR APPLICATION NUMBER: DE 19931420.9
FRIOR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Corynebacterium glutamicum
US-11-055-822-290
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US-11-054-385-12
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ORGANISM:
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US-11-124-368A-300

US-11-124-368A-300

Sequence 300, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michale Cargill

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Wascular 158A8

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-01-09

PRIOR PLING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOFTWARE: FastSEQ for Windows Version 4.0

LENTH: 555

LENTH: 555
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APPLICANT: Trueheart, Joshua
APPLICANT: Walbridge, Michael J.
APPLICANT: Walbridge, Michael J.
APPLICANT: VORGEY, PETER S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
CURRENT PELICATION NUMBER: US/10/858,730
CURRENT PILING DATE: 2004-06-01
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
PRIOR SEQ ID NOS: 364
SOFTWARE: FASSEQ for Windows Version 4.0
DB 7; Length 468;
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                                               Indels
Score 33; DB 7
Pred. No. 48;
2; Mismatches
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US-10-888-730-103
i Sequence 103, Application US/10858730
i Publication No. US20050255568A1
i GENERAL INFORMATION:
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Query Match 23.7%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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238 GPLIPSAFLGGN 249
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Query Match
Best Local Similarity
Matches 6; Conserv
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Sequence 229, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michel Cargill

APPLICANT: James J. Devlin

APPLICANT: James J. Devlin

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

FILE REFERENCE: CL001524

CURRENT APPLICATION NUMBER: US 60/568,845

PRIOR PLILING DATE: 2004-05-09

PRIOR PLILING DATE: 2004-05-07

PRIOR PLILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOCTAMARE: PSESEE for Windows Version 4.0

LENGTH: 749
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| Publication No. US20050287559A1
| Publication No. US20050287559A1
| GENERAL INFORMATION:
| APPLICANT: Michele Cargill
| APPLICANT: James J. Devlin
| APPLICANT: May Luke
| TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
| FILLE REFERENCE: CLOOLS24
| CURRENT APPLICATION NUMBER: US/11/124,368A
| CURRENT PILING DATE: 2005-05-09
| PRIOR APPLICATION NUMBER: US 60/568,845
| PRIOR APPLICATION NUMBER: US 60/625,936
| PRIOR PILING DATE: 2004-11-09
| PRIOR FILING DATE: 2004-11-09
| PRIOR FILING DATE: 2004-11-09
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46.2%; Pred. No. 79;
ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                              493 RFASALPYTTAAIGPLLP----GSATY 515
                                                                                                                                                                                                                                                                                        TYPE: PRT ; ORGANISM: Streptomyces coelicolor US-10-858-730-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 NTVKKCTKKLANF 339
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Best Local Similarity 46.2.
Best Local Similarity 6.2.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens US-11-124-368A-298
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; SEQ ID NO 103
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APPLICANT: Machine Carolina APPLICANT: May buke Tillus of Invention: Genetic Polymorphisms Associated with APPLICANT: May Luke TITLE OF INVENTION: Genetic Polymorphisms Associated with TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/658,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR PILING DATE: 2004-11-09
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 302
LENGTH: 877
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Sequence 34, Application US/10475204

Sequence 34, Application US/10475204

Sequence 34, Application US/10475204

Sequence 34, Application No. US208050277116A1

GENERAL INFORMATION:

APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION

TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE IDENTIFICATION NUMBER: US/10/475,204

CURRENT FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/285,509

PRIOR APPLICATION NUMBER: 60/285,509

PRIOR PILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 34

LENGTH: 943

TYPE: PRI

CREALISMENTEM: Homo sapiens

US-10-475-204-34
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46.2%; Pred. No. 94;
tive 2; Mismatches 5; Indels
  DB 7; Length 859;
92;
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                                                 5; Indels
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Pred. No. 1e+02;
1; Mismatches
                                                 2; Mismatches
  Score 33;
Pred. No.
                                                                                                                                                                                                           RESULT 43
US-11-124-368A-302
; Sequence 302, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
Query Match 23.7%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                          437 NTVKKCTKKLANF 449
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US-11-124-368A-302
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Sequence 1606, Application US/10793626

Publication No. US2005025478A1

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 1606
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PU3480US
CURRENT PEPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1604, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KINMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUBJ 8002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1604
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                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence US-10-793-626-670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artifitial Sequence: synthetic; CTHER INFORMATION: amino acid sequence US-10-793-626-1604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 STGGVTTSPVSGFLTPGLPGTSSWLPFGAFGSNS 115
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23.0%; Score 32; DB (Best Local Similarity 26.5%; Pred. No. 18; Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.0%;
Best Local Similarity 26.5%;
Matches 9; Conservative 3
                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Sequence 204, Application US/11052554A

Sequence 204, Application US/11052554A

Sequence 204, Application US/11052554A

Publication No. US20050288866A1

Publication No. US20050288866A1

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROJECT 2005-02-07

CURRENT FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-02-06

PRIOR FILING DATE: 2004-02-06

PRIOR FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 763

SOFTWARE: PATENTIN VERSION 3.3
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ORGANISM: Shigella flexneri 2a str. 2457T
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                                                                                                                  ; Sequence 77, Application US/11052554A; Publication No. US20050288866A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Escherichia coli 0157:H7
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25.0%;
                583 TATKGNORVOKFL 595
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Best Local Similarity 25.0°
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US-10-793-626-670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM:
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RESULT 50

US-11-194-246-104

i Sequence 304, Application US/11194246

i Publication No. US20050272089A1

GENERAL INFORMATION:

APPLICANT: Trepod, Catherine

APPLICANT: Trepod, Catherine

APPLICANT: Arvidson, Staffan

TITLE OF INVENTION: USE

FILE REFERENCE: 00592.US1 (MeR 268.05920101)

CURRENT PILING DATE: 2005-08-01

PRIOR PELICATION NUMBER: US/10/274,586

PRIOR PELICATION NUMBER: US 60/345,438

PRIOR PELING DATE: 2001-10-19

PRIOR PELING DATE: 2001-10-19

PRIOR PELING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 621

SEQ ID NO 304

LENGTH: 239
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                                                                           CTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
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                                                                                                                                                            Query Match 23.0%; Score 32; DB 6; Length 232 Best Local Similarity 26.5%; Pred. No. 35; Matches 9; Conservative 3; Mismatches 22; Indels
                                                                                                                                                                                                                                                                       3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNT 36
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Job time : 14 secs
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ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-304
                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-10-649-138-19

US-10-991-597-44

US-08-851-965-11

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Maximum Match 100%
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score greater than or equal to
and is derived by analysis of
                                                                                                                                    protein search, using
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Sequence 12, Application US/08851965

Publication No. US20020010133A1

GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: BEDULIN, Bronislava
APPLICANT: BERNON, Gareth Wyn
TITLE OF INVENTION: METHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: METHOD FOR PREVENTING
TITLE OF INVENTION: AGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: LOS ANGELES
STREET: CALIFORNIA
CITY: LOS ANGELES
STATE: CALIFORNIA
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CIP: 90017

COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT PELICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 154
ATTORNEY/AGENT INFORMATION:
NAMME: DUFY: BRADFORD J.
REGISTRATION NUMBER: 224/042
TELEPANTION INFORMATION:
TELEPHONE: 619/552-2200
TELEPAN: 211/955-0440
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 5:
CROUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,965

FILING DATE: 06-MAY-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: DUFT, BRADPORD J.

REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1,6
OTHER INFORMATION: disulfide bridge between
OTHER INFORMATION: the Cys residues
LOCATION: 36
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

84.9%; Score 118; DB 2; I
Best Local Similarity 68.6%; Pred. No. 6.9e-15;
Matches 24; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-851-965-12
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Sequence 39, Appl
Sequence 2, Appli
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; Sequence 5, Application US/08851965
; Publication No. US2002010133A1
; Publication No. US2002010133A1
; GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: GEDULIN, BETNON, Gareth Wyn
TITLE OF INVENTION: WITHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: USING AMYLIN
STILES OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-775-180-847
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CITY: LOS ANGELES STATE: CALIFORNIA COUNTRY: USA

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Gaps
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                                                                                                                                                                   Length 36;
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                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Duft, Bradford
APPLICANT: Duft, Bradford
TITLE OF INVENTION: METHODS FOR TREATING OBESITY
WIDMER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COTATION: 1,6
COTHER INFORMATION: disulfide bridge between
COTHER INFORMATION: the Cys residues
COCATION: 36
COTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-870-762A-12
                                                                                                amidated Tyr (Tyrosinamide)
                                                                                                                                                              Query Match

84.9%; Score 118; DB 2;
Best Local Similarity 68.6%; Pred. No. 6.9e-15;
Matches 24; Conservative 0; Mismatches 11.
                                                                                                                                                                                                                                                                                                      2 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                      disulfide bridge between
the Cys residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: PASSIBLE
COMPATER: PASSIBLE
CONTRIBUT
CONTRIBUT
APPLICATION DATA:
APPLICATION NUMBER: US/08/870,762A
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/870,762A
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
ATTORNEY/AGRNT INFORMATION:
NAME: DUET, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 326/104
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-552-2200
TELEFAX: 619-552-2159
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-870-762A-12; Sequence 12, Application US/08870762A; Sequence 12, Application US/030026812A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
; LOCATION: 1,6
; OTHER INFORMATION: d
; OTHER INFORMATION: t
; LOCATION: 36
; OTHER INFORMATION: a
US-08-851-965-35
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| Publication No. US20020010133A1 |
| GENERAL INFORMATION |
| APPLICANT: GEDULIN, Bronislava |
| APPLICANT: BEYNON, GATCH WA: APPLICANT: BEYNON, GATCH WA: TITLE OF INVENTION: USING AMYLIN OR AWYLIN |
| TITLE OF INVENTION: USING AMYLIN OR AWYLIN |
| ANDRESSEE: LYON & STREET |
| STREET: 633 WEST FIFTH STREET |
| CITY: LOS ANGELES |
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUET, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 32,219
TELERPAN: 213/955-0440
TELERPAN: 213/955-0440
                                                                                                                                                                                                                                                                                                           LOCATION: 1,6
OTHER INFORMATION: disulfide bridge between OTHER INFORMATION: the Cys residues LOCATION: 36
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NTATCATQRLANFLVHSSNNLGPVLPSTNVGSNTY 36
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MEDIOM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 36 amino acids TYPE: amino acid STRANDEDNESS: single
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHAX: 213/955-0440
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERESTICS:
LENGTH: 36 aming acids
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Matches 24; Conservative
                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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MOLECULE TYPE: protein
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US-08-851-965-35
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RESULT /
US-09-454-513-39
; Sequence 39, Application US/09454533
; Publication No. US20020187923A1
; Publication No. US20020187923A1
; GENERAL INFORMATION: Laura S.L. Et Al.
; APPLICANT: GAETA, Laura S.L. Et Al.
; TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; COCATION: 36
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-454-533-18
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/454,533

FILING DATE: 06-Dec-1999

CLASSIFICATION: <unhaper of the companies of th
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
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68.6%; Pred. No. 6.9e-15;
tive 0; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION UNMER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
ATONNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 213/955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                            CALIFORNIA
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Best Local Similarity 68.6<sup>1</sup>
Matches 24; Conservative
                                                                                                                                                  ZIP: 90017
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                                                                                                                                            Sequence 13. Application US/08870762A
Publication No. US20030026812A1
GENERAL INFORMATION:
APPLICANT: Duft Bradford
APPLICANT: Kolterman, Orville
TITLE OF INVENTION: METHODS FOR TREATING OBESITY
NUMBER OF SEQUENCES: 15
CORRESPONDECES: 15
CORRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 36
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 2;
Pred. No. 6.9e-15;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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      2 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disulfide bridge between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,762A
FILING DATE: 06-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RILING DATE:
PRIOR DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 226/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-2200
TELEFAX: 619-552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.9%;
68.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1,6
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 WEST CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 24;
                                                                                                                         US-08-870-762A-13
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                                                                                            RESULT 5
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
FILING DATE: Charge-2003
CLASSIFCATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/10649138

Publication No. US20040038900A1

GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION:
USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 36
OTHER INFORMATION: amidated fyr (Tyrosinamide)
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NTATXATQRLXNFLXXXXXXXXQPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.9%; Score 118; DB 4; Best Local Similarity 68.6%; Pred. No. 6.9e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
APPLICATION NUMBER: US 07/667,040 FILING DATE: 08-WAR-1991 ATORNEY/AGENT INFORMATION: NAME: DUFT, BRADFORD J. REGISTRATION NUMBER: 32,219 REFERENCE/DOCKET NUMBER: 227/006 TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 227/006 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DUFT, BRADFORD J. REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                           TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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US-10-649-138-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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STATE: COLONTRY: USA
COUNTRY: USA
ZIE: 9017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-ANG-2003
CIASSIFICATION: CURKNOW>
PRIOR APPLICATION DATA:

FRIOR APPLICATION DATA:
CIASSIFICATION DATA:
CIASSIFICATION DATA:
CIASSIFICATION DATA:
CIASSIFICATION DATA:
CONTROW APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10649138
Publication No. US200400389900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 39: US-09-454-533-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 36
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                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-NAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REPERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
FILING DATE: «UNMSNOWN»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
                                    APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 36
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Length 36;
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OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                          YOUNG, Andrew A.
RINK, Timochy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
CASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.9%; Score 118; DB 4; I ilarity 68.6%; Pred. No. 6.9e-15; Conservative 0; Mismatches 11;
                                                                                                                                                                                                          2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
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                                                                                                                                                                         3 NTATXATQRLXNFLXXXXXXXXXBPXLPXTXVGSNTY 37
                                                                                    84.9%; Score 118; DB 4; ilarity 68.6%; Pred. No. 6.9e-15; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/643,681
FILLING DATE: 18-Aug-2003
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILLING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILLING DATE: 07-SEP-193
ATTORNEY,AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                 US-10-643-681-13
Sequence 13, Application US/10643681
Sequence 13, OSCO040097415A1
Diblication No. US20040097415A1
GENERAL INFORMATION:
APPLICANT: KOLTERWAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,219
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TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: LOS ANGELES STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 24; Conserva'
                                                                                                          Local Similarity
Les 24; Conservat
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                                              US-10-643-681-6
                                                                                           Query Match
                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                    OCHER INFORMATION: amidated Tyr (Tyrosinamide); SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10643681
Publication No. US20040097415A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timochy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                        Score 118; DB 4;
Pred. No. 6.9e-15;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                            3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                              2 NTATCATQRLANFLVHSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/643,681
FILING DATE: 18-Aug-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                       LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 36 amino acids
                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            84.9%;
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 30
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                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.0-
Best Local Similarity
Conservative
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                                                                                                                                                                             FEATURE
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Length 37;
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                                                                                                                                                                                                                                                                             ZIP: 90017

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 324/042
FELEPHONE: 619/552-2200
TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-851-965-11

Sequence 11, Application US/08851965
Sequence 11, Application US/08851965
Sequence 11, Application No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: METHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: USING AMYLIN OR AMYLIN
TITLE OF INVENTION: AGONISTS
NUMBER OF SEQUENCES: 35
METHOD FOR PREVENTING GASTRITIS
USING AMYLIN OR AMYLIN
AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.9%; Score 118; DB 2; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disulfide bridge between
the Cys residues
        TITLE OF INVENTION: METHOD FOR PRITITE OF INVENTION: USING AMYLIN TITLE OF INVENTION: AGONISTS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: ADDRESSER: LYON & LYON STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: LYON & LYON
633 WEST FIFTH STREET
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                             CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 84.9%; Score 118; DB 5; Length 36 1 Similarity 68.6%; Pred. No. 6.9e-15; 24; Conservative 0; Mismatches 11; Indels
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1 Sequence 44, Application US/10991597

2 Fublication No. US20050143303A1

3 GENERAL INFORMATION:

APPLICANT: Costantino, Henry R.

TITLE OF INVENTION: INTRANASAL ADMINISTRATION OF

TITLE REPERENCE: 03-14US

CURRENT APPLICATION NUMBER: US/10/991,597

CURRENT FILING DATE: 2004-11-18

PRIOR FILING DATE: 2003-12-26

NUMBER OF SEQ ID NOS: 47

SOFTHARE: PARLSEQ for Windows Version 4.0

SEQ ID NO 44
                                                                                                                                                                                                                         APPLICANT: Quay, Steven C.
APPLICANT: Gostantino, Henry R.
TITLE OF INVENTION: INTRANASAL ADMINISTRATION OF
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
CURRENT APPLICATION NUMBER: US/10/991,597
CURRENT FILING DATE: 2004-11-18
PRIOR PILING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 36
              2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
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                                                                                                                     US-10-991-597-23
; Sequence 23, Application US/10991597
; Publication No. US20050143303A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/088519,65
Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: GEDULIN, Bronielava
APPLICANT: BEYNON, Gareth Wyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
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US-10-991-597-23
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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US-08-851-965-4
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Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: METHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: USING AMYLIN OR ARTICL
TITLE OF INVENTION: AGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32.19
REGISTRATION NUMBER: 32.19
                                                                                                                                                                                                                  LOCATION: 2,7

OTHER INFORMATION: disulfide bridge between
OTHER INFORMATION: the Cys residues
LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-851-965-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                              Query Match 84.9%; Score 118; DB 2; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: JULY,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 213/955-0440
TELEX: 67-3510
INPORMATION FOR SEQ. ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHH: 37 anino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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Sequence 13, Application US/08851965

Publication No. US20020010133A1

GENERAL INFORMATION:

APPLICANT: GEDULIN, Bronislava

APPLICANT: BEYNON, Gareth WAN

ITILE OF INVENTION: USING AMYLIN OR AMYLIN

ITILE OF INVENTION: USING AMYLIN OR AMYLIN

ITILE OF INVENTION: AGONISTS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: LYON & LYON

STREET: 633 WEST FIFTH STREET

CITY: LOS ANGELES

STATE: CALIFORNIA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLEASSIFICATION: 514
ATTORNEY/AGENT INORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 224/042
REFERENCE/DOCKET NUMBER: 224/042
TELECOMMUICATION INFORMATION:
TELEFAK: 213/955-0440
TELEFAK: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERESTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENTING STATEM TO SOFTWARE PATENTING STATEM TO SOFTWARE PATENTING DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTONENY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 224/042
TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 37
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-851-965-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NTATCATQRLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disulfide bridge between
the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
LOCATION: 2,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
US-08-851-965-13
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Query Match 84.9%; Score 118; DB 2; Length 37; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11; Indels
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GENERAL INFORMATION:
APPLICANT: Duft, Bradford
APPLICANT: ACALerman, Orville
TITLE OF INVENTION: METHODS FOR TREATING OBESITY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                               US-08-870-762A-3
; Sequence 3, Application US/08870762A
; Publication No. US20030026812A1
; GENERAL INFORMATION:
APPLICANT: Duft, Bradford
APPLICANT: Kolterman, Orville
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 37
CTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-870-762A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATQRLXNFLXXXXXXXXXCPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulfide bridge between
                                                                                                                                                                                                                                        ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/870,762A
FILING DATE: 06-UN-1997
CLASSIFICATION 1424
PROOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Cys residues
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ATTORNEY/AGENT INFORMATION:
NAME: DUPT, BRADFORD J
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-2200
TELEPAX: 619-552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                        LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2,7
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                                                                                                       Length 37;
                                                                                                  Query Match 84.9%; Score 118; DB 2; Length 37 Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/08851965
Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: GEDULIN, Bronislava
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: WEITHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
; LOCATION: 37
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-851-965-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.9%; Score 118; DB 2;
68.6%; Pred. No. 7.1e-15;
iive 0; Mismatches 11;
                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                        3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulfide bridge between
the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPLICATION NUMBER: US/08/851,965
PILING DATE: 06-MAY-1997
CLASSIFFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REPRENCE/DOCKET NUMBER: 224/042
TELECOMMUNICATION INFORMATION:
TELECHAN: 213/955-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear AOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
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Publication No. US20020187923A1

GENERAL INFORMATION:

APPLICANT: GAETA, Laura S.L. Et Al.

ITLE OF INVENTION:

USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) SEQUENCE DESCRIPTION: amidated Tyr (Tyrosinamide) (US-09-454-533-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.9%; Score 118; DB 3; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 327/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEPAX: 213/555-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILLING DATE: 06-Dec-1999
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                    FILING DATE: <Unknown>
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/892,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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Sequence No. US20020187923A1
GENERAL INFORMATION:
APPLICANT: GAETA, LAURA S.L. Et Al.
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 37
CTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-870-762A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

84.9%; Score 118; DB 2;
Best Local Similarity 68.6%; Pred. No. 7.1e-15;
Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disulfide bridge between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
                                                                                                                                 OPERATING SYSTEM: DOS
SOFTMARE: FEBLESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,762A
FILING DATE: 06-JUN-1997
CLASSIPTICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD 32,219
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 226/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-2200
TELEFAX: 619-552-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                    COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 2,7
OTHER INFORMATION:
OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: GAETA, LAURA S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
) CTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-454-533-19
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: amidated Tyr (Tyrosinamide) US-09-454-533-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 118; DB 3; 1
Pred. No. 7.1e-15;
0; Mismatches 11;
                                                                                                  Score 118; DB 3;
Pred. No. 7.1e-15;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NTATXATORLXNFLXXXXXXXXXXDEXTXVGSNTY 37
                                                                                                                                                                                    3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                          NTATCATORLANFLVRSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                         RESULT 24
US-09-454-533-21
Sequence 21, Application US/09454533
Publication No. US20020187923A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.6%;
Matches 24; Conservative 0
                                                                                               ch 84.9%;
1 Similarity 68.6%;
24; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                               Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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US-09-454-533-19
is Sequence 19, Application US/09454533
is Publication No. US20020187923A1
is FUBLICATION: MOVER STATON:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION : UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,549
FILING DATE: 10-NOV-1991
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
ATTORNEY, AGENT: NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
ATTORNEY, AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
RECHERRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: amidated Tyr (Tyrosinamide) ; US-09-454-533-17
                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                ch 84.9%; Score 118; DB 3; 1 Similarity 68.6%; Pred. No. 7.1e-15; 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXXXXCPXLPXTXVGSNTY 37
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STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  TELEPHONE: 619/552-2200
                 TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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Best Local Similarity
Matches 24; Conserva:
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Length 37;
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Publication No. US20040038900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
ATILE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.9%; Score 118; DB 4;
68.6%; Pred. No. 7.1e-15;
tive 0; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DUFT, BRADFORD J. REGISTRATION NUMBER: 32,219 REFERENCE/DOCKET NUMBER: 227/006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
                                          ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.6'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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US-10-649-138-17
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APPLICATION NUMBER: US/09/454,533 FILING DATE: 06-Dec-1999 CLASS:FICATION SUMBER: 08/99,549 FILING DATE: 06-Dec-1999 CLASS:FICATION DATA:

APPLICATION NUMBER: 08/92,549 FILING DATE: 19-NOV-1991 FILING DATE: 19-NOV-1991 APPLICATION NUMBER: US/07/667,040 FILING DATE: 19-NOV-1991 ATTORNEY/AGENT INFORMATION:

NAME: DUET, BRADFORD J. REGISCRATION NUMBER: 32,219 REFERENCE/DOCKET NUMBER: 227/006 TELEFRATION INFORMATION:

TELEFRATION: 619/552-2200 TELEFRAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/10649138
Publication No. US200400389900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GAETA, LAURA S.L. Et Al.
TITLE OF INVENTION: NOVEL AWYLIN AGONIST PEPTIDES AND
USES THEREFOR
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-454-533-38
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84.9%; Score 118; DB 3; L
Best Local Similarity 68.6%; Pred. No. 7.1e-15;
Matches 24; Conservative 0; Mismatches 11;
3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
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                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSES: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                               Sequence 38, Application US/09454533
Publication No. US20020187923A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
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                                                                RESULT 25
US-09-454-533-38
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COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE PORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEAD PC PC DOS NS - DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: amidated Tyr (Tyrosinamide)
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
84.9%; Score 118; DB 4;
Best Local Similarity 68.6%; Pred. No. 7.1e-15;
Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NTATXATQRLXNFLXXXXXXXXXBPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATCATORLANFLVRSSNNLGPVLPSTNVGSNTY 37
                    FILING DATE: 06-DEC-199
APPLICATION NUMBER: 08/892,549
FILING DATE: 4Uhrnown.
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 07/667,040
FILING DATE: 19-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFY: BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELEPHONE: 619/552-2200
TELEPHONE: 619/552-2200
TELEPHONE: 619/552-2200
TELEPHONE: 619/552-2400
TELEPHONE: 619/552-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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APPLICATION NUMBER: US/09/454;533
FILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
FILING DATE: «URKnown»
PILING DATE: «URKnown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/667,040 FILING DATE: 08-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/10649138; Publication No. US20040038900A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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Publication No. US200400389900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 4;
Pred. No. 7.1e-15;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/04/54,533
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/892,549
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US/06/67,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US/06/67,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
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ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 28
US-10-649-138-19
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Length 37;
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OTHER INFORMATION: amidated Tyr (Tyrosinamide)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                           ; CTHER INFORMATION: amidated Tyr (Tyrosinamide); SEQUENCE DESCRIPTION: SEQ ID NO: 38: US-10-649-138-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOUNG, Andrew A.
RINK, Timochy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                  3 NTATCATQRLANFLVHSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                 3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                     Query Match 84.9%; Score 118; DB 4; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/643,681
FILING DATE: 18-Aug-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO&
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/10643681
; Publication No. US20040097415A1
; GENERAL INFORMATION:
; APPLICANT: KOLTERMAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
    LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90017
COMPUTER READABLE FORM:
                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                         LOCATION:
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IDM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/649,138

FILING DATE: 26-Aug-2003

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION NUMBER: US/09/454,533

FILING DATE: 06-Dec-1999

APPLICATION NUMBER: US/09/454,533

FILING DATE: COLACOWNOW

APPLICATION NUMBER: US/09/454

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: US/09/454

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: US/09/456

FILING DATE: 19-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38, Application US/10649138
Publication No. US200400389900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                 LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.9%; Score 118; DB 4;
68.6%; Pred. No. 7.1e-15;
Live 0; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMULCATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
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ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                         INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.69
Matches 24; Conservative
                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
US-10-649-138-38
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MEDIUM ILEE: FICEPY MISH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-Aug-2003
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
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                                                                                                                YOUNG, Andrew A.
RINK, Timochy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 68.6%; Pred. No.,7.1e-15;
Matches 24; Conservative 0; Mismatches 11.
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YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
                                                                                                                                                                                                                                                   CORRESPONDENČE ADDRESS:
ADDRESSER: LYON & LYON
STREET: 633 WSST FIFTH STREET
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 205
TELECOMMUNICATION INFORMATION:
                     Sequence 14, Application US/10643681
Publication No. US2004097415A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/10643681; Publication No. US20040097415A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 37 amino acids
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INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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  US-10-643-681-14
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MEDIUM TYPES FALOPY disk

MEDIUM TYPES FALOPY disk

MEDIUM TYPES FALOPY disk

COMEVITER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 18-Aug-2003

CLASSIFICATION NUMBER: US/08/302,069A

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: 08/118,381

FILING DATE: 07-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: DUFY, BRADFORD J.

REFERENCE/DOCKET NUMBER: 209/146

TELECOMMINICATION INFORMATION:

MART: DOCKET NUMBER: 209/146
  Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.9%; Score 118; DB 4; Length 37; 68.6%; Pred. No. 7.1e-15; tive 0; Mismatches 11; Indels
                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                      APPLICANT: KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
Score 118; DB 4;
Pred. No. 7.1e-15;
0; Mismatches 11
                                                                                          3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                     NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                              Sequence 12, Application US/10643681
Publication No. US20040097415A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
    84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 68.6
Matches 24; Conservative
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    Query Match
Best Local Similarity
                                                                                                                                                                                                          RESULT 32
US-10-643-681-12
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0
                                         Length 37;
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                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Quay, Steven C.
APPLICANT: Costantino, Henry R.
TITLE OF INVENTION: INTRAMABAL ADMINISTRATION OF
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
FILE REFERENCE: 03-14US
CURRENT APPLICATION NUMBER: uS/10/991,597
CURRENT FILING DATE: 2004-11-18
PRIOR FILING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Quay, Steven C.
APPLICANT: Costantino, Henry R.
TITLE OF INVENTION: INTRANSAL ADMINISTRATION OF
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
FILE REFERENCE: 03-14US
CURRENT APPLICATION NUMBER: US/10/991,597
CURRENT FILING DATE: 2004-11-18
PRIOR APPLICATION NUMBER: 60/532,337
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FREESE FOOT FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 5;
Pred. No. 7.1e-15;
0; Mismatches 11;
                                       84.9%; Score 118; DB 5; 68.6%; Pred. No. 7.1e-15; iive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.9%; Score 118; DB 5; Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NTATXATORLXNFLXXXXXXXXXCPXLPXTXVGSNTY 37
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                                                                                                                               3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                       3 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                    Sequence 22, Application US/10991597
Publication No. US20050143303A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 24, Application US/10991597; Publication No. US20050143303A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-991-597-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-991-597-22
                  Query Match
Best Local Similarity
....heg 24; Conserve
                                                                                                                                                                                                                                                                 US-10-991-597-22
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US-10-991-597-24
US-10-991-597-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                            RESULT 36
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0
                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/643,681
FILING DATE: 18-449-2003
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: DATE OF SEP-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.9%; Score 118; DB 4; Length 37;
68.6%; Pred. No. 7.1e-15;
tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
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Sequence I. Application US/10991597

Publication No. US2005014330341

GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
APPLICANT: Costantino, Henry R.
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
CURRENT APPLICATION NUMBER: US/10/991,597
CURRENT PILING DATE: 2004-11-18
PRIOR APPLICATION NUMBER: 60/532,337
PRIOR FILING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 47
SEQTUARE: FASELSEQ for Windows Version 4.0
SEQTUARE: 37
GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                       CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 63 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                           ZIP: 90017
COMPUTER READABLE FORM:
                    SEOUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conserv
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US-10-991-597-15
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATE:

APPLICATION NUMBER: 08/892,549
FILING DATE: 4Unknown;
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 08 07/667,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUT; BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                  ZIP: 90017
COMPUTER READABLE FORM:
                CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
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Matches 24, Conserva
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Publication No. US20020187923A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                              Sequence 26, Application US/10891597
; Publication No. US20050143303A1
; GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: INTRAMASAL ADMINISTRATION OF
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
FILE REFERENCE: 03-140S
CURRENT APPLICATION NUMBER: US/10/991,597
CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: 60/532,337
PRIOR PILING DATE: 2003-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.9%; Score 118; DB 5; I Best Local Similarity 68.6%; Pred. No. 7.1e-15; Matches 24; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 5;
Pred. No. 7.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Quay, Steven C.
APPLICANT: Quay, Steven C.
APPLICANT: Costantino, Henry R.
TITLE OF INVENTION: INTRANASAL ADMINISTRATION OF TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES FILE REPERENCE: 03-140S
CURRENT APPLICATION NUMBER: US/10/991,597
CURRENT APPLICATION NUMBER: 60/532,337
PRIOR PILLING DATE: 2003-12-26
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-991-597-43; Sequence 43, Application US/10991597; Publication No. US20050143303A1; GENERAL INFORMATION:
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ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.9%;
68.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.6'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-991-597-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-991-597-43
                     US-10-991-597-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 40
US-09-454-533-11
                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 26
LENGTH: 37
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Gaps ö RESULT 41
US-10-649-139-11
Sequence 11, Application US/10649138
Publication No. US20040038900A1
GENERAL INFORMATION:
HAPPLICANT: GAETA, Laura S.L. Et Al
TITLE OF INVENTION:
USES THEREFOR Length 36; OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 11: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 84.2%; Score 117; DB 3; ilarity 68.6%; Pred. No. 1.1e-14; Conservative 0; Mismatches 11. 2 NTATCATORLANFLVHRSNNFGPILPSTNVGSNTY 36 3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37

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I CAMPEL MEDIT

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Sequence 27, Application US/08851965
Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: WOUNG, Andrew A.
APPLICANT: GEDULIN, Bronislava
APPLICANT: BEYNON, Gareth Wyn
ITILE OF INVENTION: METHOD FOR PREVENTING TITLE OF INVENTION: USING AMYLIN OR AMYLIN
TITLE OF INVENTION: AGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 MEST FIFTH STREET
CITY: LOS ANGELES
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTONENY/AGENT INPORMATION:
NAME: DUET, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 224/042
TELEPHONIS: 619/552-2200
TELEPHONIS: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: 2,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
US-09-454-533-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-851-965-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-991-597-16

Sequence 16, Application US/10991597

Publication No. US20050143303A1

GENERAL INFORMATION:

APPLICANT: Quay, Steven C.

APPLICANT: Costantino, Henry R.

TITLE OF INVENTION: INTRANASAL ADMINISTRATION OF

TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES

FILE REFERENCE: 03-14US

CURRENT APPLICATION NUMBER: US/10/991,597

CURRENT FILING DATE: 2004-11-18

PRIOR APPLICATION NUMBER: 60/532,337

PRIOR FILING DATE: 2003-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

84.2%; Score 117; DB 5; L

Best Local Similarity 68.6%; Pred. No. 1.1e-14;

Matches 24; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%; Score 117; DB 4;
68.6%; Pred. No. 1.1e-14;
tive 0; Mismatches 11
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             PILING DATE: 26-Aug-2003
PILING DATE: 26-Aug-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA: abplication DATA: abplication NUMBER: US/09/454,533
PILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
FILING DATE: cUnknown>
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US/07/667,040
FILING DATE: 08-NAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADDFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 327/006
TELECOMMUNICATION:
APPLICATION NUMBER: US/10/649,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 68.6
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-991-597-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-649-138-11
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LENGTH: 36
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Matches
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                                                                                                                                Length 37;
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Publication No. US20020187923A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                               Indels
                                            LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                   84.2%; Score 117; DB 2;
68.6%; Pred. No. 1.1e-14;
cive 0; Mismatches 11
                                                                                                                                                                                                                            3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                               NTATCATORLINELVRSSHNLGPALPPTDVGSNTY 37
disulfide bridge between
the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSE
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 37
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-649-138-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 18-Aug-2003

CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTATCATORLTNFLVRSSHNLGPALPPTDVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
                                                         APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
APPLICATION NUMBER: 08/892,549
                                                                                                                                                                        FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/10643681
Publication No. USZO040097415A1
GENERAL INFORMATION:
APPLICANT KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REPERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 30
CLASSIFICATION: <U PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roPoLoGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-643-681-28
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Publication No. US20040038900A1
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.2%; Score 117; DB 3; Length 37; Best Local Similarity 68.6%; Pred. No. 1.1e-14; Matches 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/649,138
FILING DATE: 26-Aug-2003
                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: <university control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION INMBER: 227/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 37 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                 ZIP: 90017
COMPUTER READABLE FORM:
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STATE: CALIFORNIA
COUNTRY: USA
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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Query Match 83.5%; Score 116; DB 2; Length 36; Best Local Similarity 68.6%; Pred. No. 1.7e-14; Matches 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAMSR: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 36
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-851-965-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NTATCATORLANFLVRSSNNFGPILPPTNVGSNTY 36
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the Cys residues
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Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: GEDULIN, Bromislava
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: METHOD FOR PREVENTING
TITLE OF INVENTION: AGNISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
CONTRACTOR OF ADDRESSEE: LYON & LYON
AGNISTATION ADDRESSEE: LYON & LYON
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224/042
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: LYON & LYON
633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 224/
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEPAX: 213/955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1,6
OTHER INFORMATION:
OTHER INFORMATION:
                                                                     CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOS ANGELES
CALIFORNIA
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                                                                                                 STATE: CA
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84.2%; Score 117; DB 4; Length 37;
Best Local Similarity 68.6%; Pred. No. 1.1e-14;
Matches 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.2%; Score 117; DB 5; Length 37; 68.6%; Pred. No. 1.1e-14; ive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: amidated Tyr (Tyrosinamide) ; SEQUENCE DESCRIPTION: SEQ ID NO: 28: US-10-643-681-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08851965
Publication No. US20020010133A1
GENERAL INFORMATION:
APPLICANT: YOUNG, Andrew A.
APPLICANT: GEDULIN, Bronislava
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: WETHOD FOR PREVENTING GASTRITIS
TITLE OF INVENTION: USING AMYLIN OR AMYLIN
TITLE OF INVENTION: AGONISTS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Quay, Steven C.
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION: GLUCOSE-REGULATING PEPTIDES
TITLE OF INVENTION NUMBER: US/10/991,597
CURRENT APPLICATION NUMBER: 60/532,337
PRIOR PILING DATE: 2004-11-18
PRIOR FILING DATE: 2003-12-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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               NAME: DUPT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE\DOCKET NUMBER: 209/146
TELECOMUNICATION INFORMATION:
TELEFAX: 213/955-0200
TELEFAX: 213/955-0440
TELEFAX: 213/955-0440
INFORMATION FOR SEQ 1D NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/10991597 Publication No. US20050143303A1 GENERAL INFORMATION:
       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 24; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-991-597-38
                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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US-08-851-965-8
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LENGTH: 36 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.5%; Score 116; DB 2; Length 36 Best Local Similarity 68.6%; Pred. No. 1.7e-14; Matches 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-851-965-18

Sequence 18, Application US/08851965

Publication No. US2002010133A1

GENERAL INFORMATION:
APPLICANT: GEDULIN, Bronislava
APPLICANT: BEYNON, Gareth Wyn
TITLE OF INVENTION: USING AMYLIN OR AMYLIN
STITLE OF INVENTION: ACONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USAN
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUTY, BRADFORD J.
REGISTRATION NUMBER: 224/042
FELECOMMUNICATION NUMBER: 224/042
TELECOMMUNICATION NUMBER: 224/042
TELEFRAX: 213/955-0440
TELEFRAX: 213/955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1,6
COTHER INFORMATION: disulfide bridge between
COTHER INFORMATION: the Cys residues
LOCATION: 36
COTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-851-965-9
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                 FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUET, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 224/042
TELEPHONE: 619/552-220
TELEPAX: 213/955-0440
TELEPAX: 213/955-0440
TELENA: 67-3510
INFORMATION FOR SEQ ID NO: 9: SEQUENCE GHARACTERISTICS:
LENGTH: 36 amino acid
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRATURE:
APPLICATION NUMBER: US/08/851,965
FILING DATE: 06-MAY-1997
CLASSIFICATION: 514
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Q6nu42 xenopus lae
Q5u9g5 aspergillus
Q4wjt8 aspergillus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                    giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUCLEOTIDE SEQUENCE.
MEDLINE=89345542; PubMed=2668946;
Nishi M., Chan S.J., Nagamateu S., Bell G.I., Steiner D.F.;
"Conservation of the sequence of islet amyloid polypeptide in five mammals is consistent with its putative role as an islet hormone.";
Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-Ept amyloid polypeptide precursor (Diabetes-associated peptide)
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OSZVP2_LEGPH
O8PWN3_METMA
O6VZ92_CNPV
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Q6N445_RHOPA
Q55N48_CRYNE
OXAA_PSESM
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                      971431 LEPDI
Q7XPC9 ORYSA
Q8V1S0 9HEPC
Q8V1S1 9HEPC
Q8V1S2 9HEPC
                                                                      Q8V1S5_9HEPC
Q8V1S5_9HEPC
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06XQ71 SACKL
064935 9CORO
08BTX1 LACPL
05V824 HALMA
05WWV0 LEGPL
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PROMM
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Q6FNQ3_CANGA
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Q7QS13_GIALA
Q6BU31_DEBHA
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9VIRU
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QSKK38 CRYN
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POLG EC16H
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PYRD PRC
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REALINE-STREAMS SCHOOL FARMS .

STRAIN-CSTREAMS SCHOOL SCHOOL STRAIN-CSTREAMS .

STRAIN-CSTREAMS .

RELINE-2238257. PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunzatne P.H.,

Rosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunzatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Schwultz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Marzy D.W., Marzy M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., McEwa R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-89325677; PubMed-2666169; DOI=10.1016/0014-5793(89)81467-X; Betsholtz C., Christmansson L., Engstroem U., Rorsman F., Svensson V., Johnson K.H., Westermark P.; "Sequence divergence in a specific region of islet amyloid polypeptide (IAPP) explains differences in islet amyloid formation between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 231.264(1989).
--- FUNCTION: Selectively inhibits insulin-stimulated glucose
--- utilization and glycogen deposition in muscle, while not affecting
adipocyte glucose metabolism.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the calcitonin family.
                                       STRAIN=DBA/2J; TISSUE=Liver; MEDLINE=97424750; PubMed=9278863; DOI=10.1677/jme.0.0190079; Ekawa K., Nishi M., Ohagi S., Sanke T., Nanjo K.; "Cloning of mouse islet amyloid polypeptide gene and characterization of its promoter."; J. Mol. Endocrinol. 19:79-86(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Islet amyloid polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M25389; AAA37874.1; -; mENA.
EMBL; D31820; BAA22051.1; -; Genomic_DNA.
EMBL; BC027527; AAH27527.1; -; mENA.
                                                                                                                                                     J. Mol. Endocrinol. 19:79-86(1997).
[3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
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FEBS Lett. 2
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MEDLINE=89325677; PubMed=266169; DOI=10.1016/0014-5793(89)81467-X;
Betsholtz C., Christmanseon L., Engstroem U., Rorsman F., Svensson V., Johnson K.H., Westermark P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WAP; TISSUE=Liver;

MEDLINE=91027936; PubMed=2223885; DOI=10.1016/0167-4781(90)90210-S; van Mansfeld A.D.M., Mosselman S., Hoeppener J.W.M., Zandberg J., van Teeffelen H.A.M., Baas P.D., Lips C.J.M., Jansz H.S.; "Islet amyloid polypeptide: structure and upstream sequences of the IAPP gene in rat and man.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishi M., Chan S.J., Nagamateu S., Bell G.I., Steiner D.F.; "Conservation of the sequence of islet amyloid polypeptide in five mammals is consistent with its putative role as an islet hormone."; Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89240689; PubMed-2654937;
Leffert J.D., Newgard C.B., Okamoto H., Milburn J.L., Luskey K.L.;
"Rat amylin: cloning and tissue-specific expression in pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-MAY-2005 (Dispeptide precursor (Diabetes-associated peptide)
                     Tyrosine amide (G-75 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Regional distribution and molecular forms of rat islet amyloid
                                                                                                                                                                                    ;
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BEDLINE-90026410; PubMed=2679555;
ABai J., Nakazato M., Kangawa K., Matsukura S., Matsuo H.;
"Isolation and sequence determination of rat islet amyloid
                                                                                                                                      Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90290528; PubMed=2357234;
Asai J., Nakazato M., Miyazato M., Kangawa K., Matsuo H.,
                                                                                                                                                                                    0; Mismatches 11; Indels
                                           group).
By similarity.
B135DBBC81475B15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:3127-3130(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lochem. Biophys. Res. Commun. 164:400-405(1989).
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                                                                                                                                      Score 116; DB 1;
Pred. No. 1.7e-14;
                                                                                                                                                                                                                                3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                     40 NTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                    44
10022 MW;
                                                                                                                                                            (89.89
                                                                                                                                      83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 38-74.
                                                                                                                                                                                    24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                 39
93 AA;
                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Amylin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsukura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Iapp
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               IAPP RAT
PROPEP
MOD_RES
                                                                    DISULFID
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             islets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DAP)
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                   RESULT 2
IAPP_RAT
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                                                                                                                              "Sequence divergence in a specific region of islet amyloid polypeptide (IAPP) explains differences in islet amyloid formation between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE-91155952; PubMed=2293024;
Nishi M., Steiner D.F.;
"Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and glucagon precursors from a New World rodent, the degu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Octodon degus (Degu).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Hystricognathi, Octodontidae, Octodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine amide (G-75 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00113; CALCITONIN; 1.
PROSTIES: PS00258; CALCITONIN; 1.
Amidation; Amyloid; Cleavage on pair of basic residues;
Direct protein sequencing; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Islet amyloid polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y similarity.
5A76C92E624DA962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 116; DB 1;
Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S13566; TCRTIA.
Ensembl; ENSRNGG00000012417; Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M25390; AAA41359.1; -; mRNA.
EMBL; J04544; AAA40730.1; -; mRNA.
EMBL; X52820; CAA37003.1; -; Genomic_DNA.
EMBL; X52821; CAA37003.1; JOINED; Genomic_DNA.
PIR; $13566; TCRTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
15-let amyloid polypeptide precursor (Amylin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 NTATCATQRLANFLVRSSNNLGPVLPPTNVGSNTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfan; PF00214; Calc CGRP IAPP; T.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 44
93 AA; 10015 MW;
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68.6%;
                                                                       species.";
FEBS Lett. 251:261-264(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGD; 2854; Iapp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAPP_OCTDE
AC
P22889;
DT 01-AUG-1991
DT 01-AUG-1991
DT 10-MAY-2005
DE 181et amyloi
GN Name=1APP;
OS OCTOGON degu
OC Hystricognat
OX NCBI_TAXID=1
RN [1]
RN [
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SEQUENCE
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37 AA; 3921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similaricy
hes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAPP MESAU
                                                                                                                                                                                                                                                                                                                               MOD RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                    removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
SPTT WE BEEN WAS A STATE OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89325677; PubMed=2666169; DOI=10.1016/0014-5793(89)81467-X; Betsholtz C., Christmansson L., Engstroem U., Rorsman F., Svensson V., Johnson K.H., Westermark P.; Specific region of islet amyloid polypeptide (IAPP) explains differences in islet amyloid formation between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting addipocyte glucose metabolism.

SUBCELLULAR LOCATION: Secreted.
SIMIKARITY: Belongs to the calcitonin family.
                                                        utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Cricetidae, Cricetinae, Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine amide (G-74 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amidation; Amyloid; Cleavage on pair of basic residues; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                   Mol. Endocrinol. 4:1192-1198(1990).
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 109; DB 1; Length 91
Pred. No. 3.9e-13;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Islet amyloid polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
42AB31AE1CE9EA99 CRC64;
                                                                                                                        SIMILARITY: Belongs to the calcitonin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FRB-1991 (Rel. 17, Last sequence update)
15-10-MAY-2005 (Rel. 47, Last annotation update)
15-16-16 amyloid polypeptide (Amylin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 AA
                                                                                                                                                                                                                                                                                   EMBL, M57669; AAA40589.1; -; mRNA.
PTR; A36118; A36118.
InterPro: IPR000443; Amylin.
InterPro: IPR001699; Calcitonin-like.
InterPro: IPR002163; Calcitonin B.
Pfam; PR00214; Calc CaRP IAPP; I.
PRINTS; PR00819; CALCITONINB.
PRINTS; PR00818; ISEETAMYLOID.
SMART; SM00113; CALCITONIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cricetulus griseus (Chinese hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group)
By sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00258; CALCITONIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%;
65.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 65.7
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
34
73
91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AA;
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    degus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species.'
FEBS Lett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Cricetidae; Cricetinae; Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91067499; PubMed-2251153;
Nishi M., Bell G.I., Steiner D.F.;
"Sequence of a cDNA encoding Syrian hamster islet amyloid polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56067; CAA39545.1; -; mRNA.
PIR; 513116; S1116.
InterPro; IPR0010443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin B.
Fam; PP00214; Calc CGFP IARP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SWART; SM00113; CALCITONIN; 1.
PROSTITE; P500258; CALCITONIN; 1.
Amyloid; Cleavage on pair of basic residues; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%; Score 107; DB 1; Length 37; 65.7%; Pred. No. 3.5e-13; tive 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
FE433D9905EBF82E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
laste amyloid polypeptide precursor (Amylin).
Name=1APP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NTATCATQRLANFLVHSNNNLGPVLSPTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tyrosine amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AA
                                                                                                                                                                                       PIR; S05037; S05037.

InterPro; IPR000443; Amylin.

InterPro; IPR001693; Calcitonin-like.

InterPro; IPR002163; Calcitonin B.

Pfam; PP00214; Calc CGRP IAPP; I.

PRINTS; PR00817; CALCITONINB.

PRINTS; PR00818; ISLEAMYLOID.

SMART; SW00113; CALCITONIN; 1.

PROSITE; PS00258; CALCITONIN; 1.

Amidation; Amyloid; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus auratus (Golden hamster).
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noumo apprens, notaman, Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metaroa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90306394; PubMed=2365085; DOI=10.1016/0014-5793(90)80314-9; Christmanson L., Rorsman F., Stenman G., Westermark P., Beteboltz C.; "The human islet amyloid polypeptide (IAPP) gene. Organization, chromosomal localization and functional identification of a promoter
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89034228; PubMed=3053705; Sanke T., Bell G.I., Sample C., Rubenstein A.H., Steiner D.F.; Mhn islet amyloid peptide is derived from an 89-amino acid precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90114181; PubMed=2608057; Rishi M., Sanke T., Seino S., Eddy R.L., Fan Y.-S., Byers M.G., Shows T.B., Bell G.I., Steiner D.F., "Human islet amyloid polypeptide gene: complete nucleotide sequence, chromosomal localization, and evolutionary history."; Mol. Endocrinol. 3:1775-1781(1989).
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE 91027936; PubMed=2223885; DOI=10.1016/0167-4781(90)90210-S; van Mansfeld A.D.M., Mosselman S., Hoeppener J.W.M., Zandberg J., van Teeffelen H.A.A.M., Baas P.D., Lips C.J.M., Jansz H.S.; "Islet amyloid polypeptide: structure and upstream sequences of the IAPP gene in rat and man."; Blicchim. Blophys. Acta 1087:235-240(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89211434; PubMed=2651160; DOI=10.1016/0014-5793(89)81260-8; Mosselman S., Hoeppener J.W.M., Lips C.J.M., Jansz H.S.; "The complete islet amyloid polypeptide precursor is encoded by two
                                                                                                                                                                                                                                                                                                                                                                                                                                     P10997; Q14598;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Islet amyloid polypeptide precursor (Diabetes-associated peptide)
(DAP) (Amylin) (Insulinoma amyloid peptide).
                                                                                               Tyrosine amide (G-74 provides amide
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                 Length 92;
                                                                                                                                                                                                                                        12; Indels
                                                          Islet amyloid polypeptide.
                                                                                                                                    By similarity.
6D2F7359C4A1D029 CRC64;
                                                                                                                                                                                            Score 107; DB 1;
Pred. No. 9.9e-13;
0; Mismatches 12
                                                                                                                                                                                                                                                                           3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                             39 NTATCATQRLANFLVHSNNNLGPVLSPTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                         89 AA
                      Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic processing.";
Biol. Chem. 263:17243-17246(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region.";
FEBS Lett. 267:160-166(1990)
                                                                                                                                                                                                 77.0%;
65.7%;
                                                                                                                                                         9899 MW;
                                                                                                                                                                                                                                        23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                    22
34
73
73
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                     Similarity
                                                                                                                                                         92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=IAPP
                                                                                                                                      DISULFID
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                       Local
                                                        PEPTIDE
                                                                                               MOD_RES
                    SIGNAL
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IAPP HUMAN
IAPP HUMAN
IAC DIO97/20
DT 01-UUL-
DT 10-MALIN
DE (DAB)
GN NAME=11
GN NAME=11
GN NAME=11
COC MAMMALIN
RP MEDLIN
RA MOSSELIN
RA MEDLIN
RA SANWS
RT "THE CALONC
RA SANWS
RT "THE RESIN RA CALIST
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  Signal
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REMIDINES-911225; phubMed-192806; phubMed-192806; Manner H.S.; Amaner H.S.; Hopepener J. H.M.; Jispe C.J.H.; Amaner H.S.; Amaner H.S.; Hopepener J.H.; Hopepener H.S.; Hopepener J.H.; Hopepener H.S.; Hopepener J.H.; H
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[1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        89 AA;
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PROPEP
MOD RES
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use as long as its content is in no way modified and this statement is not
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Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                  amide
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                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine amide (G-71 provides
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Pred. No. 9.2e-12;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
S -> G (in dbSNP:1800203).
/FTIGHVAR_012080.
S -> C (in Ref. 4; CRA39504).
AA8B1F7FD9FCB4BD CRC64;
                                                                                                                                                                                                                                                                                                                                    Direct protein sequencing; Hormone; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                      SMART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
Amidation; Amyloid; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                               Islet amyloid polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 NTATCATQRLANFLVHSSNNFGAILSSTNVGSNTY 70
                                                                                                   AAA35983.1; -; Genomic_DNA.
CAA37002.1; -; Genomic_DNA.
CAA37002.1; JOINED; Genomic_DNA.
                                                                                                     EMBL; M26650, AAA35983.1; -; Genomic_DNA.

EMBL; X52818; CAA37002.1; -; Genomic_DNA.

EMBL; X52819; CAA37002.1; JOINED; Genomic_DNA.

EMBL; X5630; CAA39504.1; -; Genomic_DNA.

EMBL; X5634; CAA39504.1; -; Genomic_DNA.

EMBL; X58830; CAA48724.1; -; Genomic_DNA.
                                                                                                                                                                 Encembl. SNUGGOOGO121351; Homo sapiens.
BRNGGOOGO121351; Homo sapiens.
HGNC; HGNC:5329; IAPP.
MIM; 147940; .
GO; GO:0005525; C:Soluble fraction; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007267; P:signal transduction; TAS.
InterPro; IPR000443; Amylin.
InterPro; IPR0001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin-like.
InterPro; PR00114; Calc CGRP IAPP; I.
PRINTS; PR00014; Calc CGRP IAPP; I.
PRINTS; PR00014; CALCITOWINE.
SMART; SM00113; CALCITOWINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG, 1990 (Rel. 15, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-FBB-1995 (Rel. 47, Last annotation update)
1slet amyloid polypeptide precursor (Amylin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 AA.
                                                      Genomic_DNA.
Genomic_DNA.
Genomic_DNA.
                                                                                             Genomic DNA
                            Genomic_DNA
                                                                                                                                                                                                                                                                                                                                             Potential
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                                                                                                                                                                                                                                                                                                                                                                                            group)
                                                                                    mRNA
                                                      CAB57804.1; -; CAB57804.1; -; CAB57803.1; -; CAB5781.1; -; CAB5781.1; -; n
                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         9806 MW;
                                                                                             AAA51728.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 62.9
22; Conservative
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53
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                                                                                                                                                             PIR; S04016; TCHUIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AA;
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                            EMBL; M27503;
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                                                         X14902;
                                                                  X14903;
                                                                          X13859;
                                                                                    J04422;
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            removed
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P17716;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                             MEDIINE 9020487; PubMed-202009;
Jordan K., Murtaugh M.P., O'Brien T.D., Westermark P., Betsholtz C., Johnson K.H.;
Jordan K.H.; Murtaugh M.P., O'Brien T.D., Westermark P., Betsholtz C., Johnson K.H.;

"Canine IAPP CDNA sequence provides important clues regarding diabetogenesis and amyloidogenesis in type 2 diabetes.";

Biochem Biophys. Res. Commun. 169:502-508(1990).

-I. FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.

-I. SUBCELLULAR LOCATION: Secreted.
-I. SUBCELLULAR: Delongs to the calcitonin family.
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REMBL; M37720; AAA30849.1; -; mRNA.

REL; M37720; AAA30849.1; -; mRNA.

RELSembl; SECATOO000012365; Canis familiaris.

RICEPPO; IPRO00443; Amylin.

RICEPPO; IPRO01693; Calcitonin-like.

RICEPPO; IPRO01693; Calcitonin-B.

REPRINTS; PRO0817; CALCITONINB.

REPRINTS; PRO0817; CALCITONINB.

REPRINTS; PRO0819; CALCITONIN 1.

REPROSTIE; PS00289; CALCITONIN; 1.

REPROSTIE; PS00289; CALCITONIN; 1.

REPROSTIE; PS00289; CALCITONIN; 1.

REPROSTIE; PS00289; CALCITONIN; 1.
MEDLINE=92182022; PubMed=1543754; DOI=10.1016/0167-4781(92)90470-K; Albrandt K., Mull E., Cooper G.J.S., Johnson M.J.; "Nucleotide sequence of a cDNA for canine amylin."; Biochim. Biophys. Acta 1130:97-99(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrosine amide (G-71 provides amide
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Pred. No. 2.3e-11;
0; Mismatches 13; Indels
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By similarity.
S -> T (in Ref. 2).
9BF757EIC1493EEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37
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01-0CT-1989 (Rel. 12, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Islet amyloid polypeptide precursor (Amylin).
Name=1APP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY
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                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 43-68
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62.9%;
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Best Local Similarity 62.9'
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01-NOV-1996
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                                                                                                                                                                                                                               diabetic cat are derived from a neuropeptide-like protein also present in normal islet cells.";
Proc. Natl. Acad. Sci. U.S.A. 84:3881-3885(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diabetes 39:118-122(1990).
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                             MEDLINE=87231921; PubMed=3035556;
Westermark P., Wernstedt C., Wilander E., Hayden D.W., O'Brien T.D.,
                                                                                                                                                                                                             "Amyloid fibrils in human insulinoma and islets of Langerhans of the
               Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.; "Conservation of the sequence of islet amyloid polypeptide in five mammals is consistent with its putative role as an islet hormone."; Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 34-70.
MEDLINE=91006862; PubMed=2210054;
MEDLINE=91006862; PubMed=2210054;
MESTANDE C., Christmanson L., Engstrom U., Rorsman F., Jordan K., O'Brien T.D., Murtaugh M., Johnson K.H., Westermark P.;
"Structure of cat islet amyloid polypeptide and identification of amino acid residues of potential significance for islet amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine amide (G-71 provides amide
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Pred. No. 2.3e-11;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00258; CALCITONIN; 1.
Amidation; Amyloid; Cleavage on pair of basic residues;
Direct protein sequencing; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Islet amyloid polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group).
By similarity.
0834D783DEAD72A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adipocyte glucose metabolism.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the calcitonin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Islet amyloid polypeptide precursor (Amylin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfam; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M25388; AAA30813.1; -; mRNA.
MEDLINE=89345542; PubMed=2668946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00113; CALCITONIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9832 MW;
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                                                                                                                           PROTEIN SEQUENCE OF 34-50
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Matches 22; Conservative
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89 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   formation.":
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01-OCT-1989
                                                                                                                                                                                           Johnson K.H.
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ID _IAPP_CAVE
AC P12966;
DT 01-0CT-15
DT 10-MAY-20
DE ISlet amy
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RRYRY RYRY RRYRY R
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                      MEDLINE=89345542; PubMed=2668946;
Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.;
"Conservation of the sequence of islet;amyloid polypeptide in five mammals is consistent with its putative role as an islet hormone.";
Proc. Natl. Acad. Sci. U.S.A. 86:5738-9742(1989).
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the calcitotin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gallifofmes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine amide (G-74 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage on pair of basic residues; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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MEDLINE=95021303; PubMed=7935487; DOI=10.1210/me.8.6.713;
Fan L., Westermark G., Chan S.J., Steiner D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 92;
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Cavia porcellus (Guinea pig).
Bukaryote; Meteazoa; Chordata; Craniata) Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Islet amyloid polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
67F3629014BF3F9C CRC64;
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Last annotation update)
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0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfan; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SMART; SM00113; CALCITONIN; 1.
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InterPro; IPR000443; Amylin.
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Q90743;
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nes 22; Conservative
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                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
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                                                                                                             NCBI_TaxID=10141;
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Gaps

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Indels

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Mismatches

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                                                                                                                                                                           Q4TB97_TETNG PRELIMINARY;
Q4TB97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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Matches 17;
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                                                                                                                                                                                                                                                                                                                              (Fragment)
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SEQUENCE
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      Matches
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Mammalia, Eutheria, Laurasiatheria, Insectivora, Erinaceidae,
Erinaceinae, Erinaceus.
"Altered gene structure and tissue expression of islet amyloid polypeptide in the chicken."; Mol. Bendorition. 8:713-721(1994). EMBL; L16955; AAA67704-1; -; mRNA. PIR; A56855; A56855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                               Ensembl; ENSGALGOODO013168; Gallus gallus.

R GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0005576; C:extracellular region; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004672; F:protein kinase activity; IEA.

R GO; GO:0004672; F:protein amino acid phosphorylation; IEA.

R GO; GO:000468; P:protein amino acid phosphorylation; IEA.

R GO; GO:000468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00163; Calcitonin_B:

InterPro; IPR00163; Calcitonin_B:

InterPro; IPR00163; Calcitonin_B:

InterPro; IPR00119; Prot_Kinase.

R PRINTS; PR00811; CALCITONINB.

R PRINTS; PR00818; ISLETAMYLOID.

R PRANTS; SM00113; CALCITONIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87; DB 2; Length 13., Pred. No. 1.3e-08;
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Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
van Dijk M.A.M., de Jong W.W.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van Dijk M.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amyloid protein.
83DE3223AC735159 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| ||||| :||
82 NTATCVTQRLADFLVRSSSNIGAIYSPINVGSNTY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=iapp;
Erinaceus europaeus (Western European hedgehog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 AA
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00258; CALCITONIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
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InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin-B.
Pfam; PF00214; Calc CGRP IAPP; T.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00258; CALCITONIN; 1.
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58.1%;
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Q9BEFO;
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les 19; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Lagomorpha, Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF7172, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EWBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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51 AA; 5599 MW; 2AB836DCCCB4BBEF CRC64;
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Pred. No. 3.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
EMBL, CAAE01007172; CAF89835.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAPP RABIT STANDARD; PRT; 67 AA. 007334; Q28741; Q9BED7; 15-JUL-1998 (Rel. 36, Created) 15-BFB-2003 (Rel. 41, Last sequence update) 10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                               51 AA.
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3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVG 33
                                                         36 NTATCATORLVNFLSRSSNNLGAILSPTDVG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                            PRT;
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EMBL; U62627; AAB05918.1; -; Genomic_DNA.
         NCBI_TaxID=9823;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED suststation the European Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                      -I. FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.
-I. SUBCELLULAR LOCATION: Secreted.
-I. SIMILARITY: Belongs to the calcitonin family.
                                                                                                                                                                                 MEDLINE=93215963; PubMed=8462765; DOI=10.1007/BF00399947; Christmanson L., Betsholtz C., Leckstroem A., Engstroem U., Cortie C., Johnson K.H., Adrian T.E., Westermark P.; "Islet amyloid polypeptide in the rabbit and European hare: studies on its relationship to amyloidogenesis."; Diabetologia 36:183-188(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                NUCLEOTIDE SEQUENCE OF 1-66.
van Dijk M.A.M., de Jong W.W.;
"Indels indicate that rodents are monophyletic and lagomorphs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00258; CALCITONIN, PARTIAL.
Amyloid; Cleavage on pair of basic residues; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 1; Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Indels
                                                                   their sister group.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Albrandt K., Sierzega M.B., Mull B., Brady E.M.G., "PCR amplification of amylin 3-34 from genomic DNA."; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Islet amyloid polypeptide By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BFSFEC2064F69646 CRC64;
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0; Mismatches
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15-UUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Islet amyloid polypeptide (Amylin) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ286814; CAC28529.1; -; mRNA.
EMBL; U66530; AAB05917.1; -; Genomic_DNA.
EMBL; S57804; AAB26084.1; -; mRNA.
FIR; 146634; 146934.
InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
PRINTS; PR00818; ISLETAMTACID.
SWART; SM00113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 42-64. STRAIN=New Zealand white;
                                                                                                     NUCLEOTIDE SEQUENCE OF 36-67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AA;
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            NCBI_TaxID=9986;
  Oryctolaque
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Q29119;
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                        Albrandt K., Sierzega M.E., Mull E., Brady E.M.G.;
"PCR amplification of amylin 3-34 from genomic DNA.";
"PCR amplification of amylin 3-34 from genomic DNA.";
Submitted (AUG-1996) to the BMBL/GenBank/DDBJ databases.
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
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"PCR amplification of amylin 3-34 from genomic DNA.";
"PCR amplification of amylin 3-34 from genomic DNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose
utilization and glycogen deposition in muscle, while not affecting
adipocyte glucose metabolism.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
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Mammalia; Butheria; Buarchontoglires; Primates; Platyrrhini;
Callitrichidae; Saguinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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10-MAY-2005 (Rel. 47, Last annotation update)
18let amyloid polypeptide (Amylin) (Fragment).
Name=IAPP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00214; CALC CGRP IAPP; 1.
PRINTS; PR00818; ISLETAMYLOID.
SMART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 AA; 3466 MW;
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hes 16; Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amyloid; Hormone.
PEPTIDE <1
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2 TATCETORLANFLAPSSNKLGAIFSPTKMG$ 32
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Matches
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                                                                                         RESULT 17
                                                                                                                    CALCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albrandt K., Sierzega M.E., Mull E., Brady E.M.G.;
"PCR amplification of amylin 3-34 from genomic DNA.";
"PCR amplification of amylin 3-34 from genomic DNA.";
Submitted (AUG-1996) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose
utilization and glycogen deposition in muscle, while not affecting
adipocyte glucose metabolism.
-!- SUBCELLULAR LOCATION: Secreted.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
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                                                                                                                                                                                                                                                                                                                                                        91A219AEE3882C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the calcitonin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 47, Last annotation update)
18let amyloid polypeptide (Amylin) (Fragment).
Name=IAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NTATCSMHRLADFLGRSSNNFGAILSPTNVGS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGS 34
                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 1
Pred. No. 0.000
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AA
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InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR000443; Amylin.
InterPro; IRR0016543; Calcitonin-like.
InterPro; IRR002163; Calcitonin B.
Pfam; PF00214; Calc. CGRP_IAPP; I.
PRINTS; PR00614; CALC. TTONINB.
PRINTS; PR00618; ISLETAMYLOID.
SWART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; PARTIAL.
Amyloid; Hormone. >32 Islet amylo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00258; CALCITONIN; PARTIAL. Amyloid; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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PRINTS; PR00818; ISLETAMTLOID.
SMART; SM00113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                           3340 MW;
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3300 MW;
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 46.9
Les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                           32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAPP SHEEP
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NON TER
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NON TER
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      SO RECENT OF THE SOLUTION SOLU
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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Phenylalanine amide (G-107 provides amide
                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 70-106, CHARACTERIZATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=20148807; PubMed=10681586; DOI=10.1074/jbc.275.8.5934; Seon A.A., Pierre T.N., Redeker V., Lacombe C., Delfoux A., Nicolas P., Amiche M.; Nicolas P., Amiche M.; Nicolas P., Amiche M.; Structure, synthesis, and activity of a new member of the calcitonin gene-related peptide family from frog skin and molecular cloning of its precurence."; Diaol. Chem. 275:5934-5940(2000).
--- FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxypeptidase.
Skin calcitonin gene-related peptide.
Removed in mature form by an
                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Skin calcitonin gene-related peptide precursor (S-CGRP).
Phyllomedusa bicolor (Two-colored leaf frog).
Phyllomedusa bicolor (Two-colored classes frog).
Amphibia; Batrachia; Annura; Neobatrachia; Hyloidea; Hylidae;
Phyllomedusinae; Phyllomedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin, intestine and brain.
-!- MASS SPECTROMETRY: MW=3806.77; METHOD=MALDI; RANGE=70-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Removed in mature form by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the calcitonin family.
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72 DTSTCATQRLADFLSRSGGIGSPDFVPTDVSANSF 106
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Amidation; Cleavage on pair of basic residues;
Direct protein sequencing; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.7%; Score 58; DB 1;
37.1%; Pred. No. 0.0055;
iive 6; Mismatches 16
115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y18495; CAB76385.1; -; MRNA.
InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfam; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00814; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SMART; SM00113; CALCITONIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                        SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                NCB1_TaxID=8393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin;
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   PHYBI
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4 TATXATORLXNFLXXXXXXXXXGPXLPXTXVGS 34

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                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                    Albrandt K., Sierzega M.E., Mull E., Brady E.M.G.;
"PCR amplification of amylin 3-34 from genomic DNA.";
"PCR amplification of amylin 3-34 from genomic DNA.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Selectively inhibits insulin-stimulated glucose
utilization and glycogen deposition in muscle, while not affecting
adipocyte glucose metabolism.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50; DB 1; Length 32;
Pred. No. 0.048;
1; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Islet amyloid polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 AA; 3247 MW; 9A5709394BB44C19 CRC64;
10-MAY-2005 (Rel. 47, Last annotation update) Islet amyloid polypeptide (Amylin) (Frågment) Name=IAPP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-Calitonin gene-related peptide (CGRP).
Rana ridibunda (Laughing frog) (Marsh frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U62626; AAB05915.1; -; Genomic_DNA.
InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00258; CALCITONIN; PARTIAL. Amyloid; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00214; Calc CGRP IAPP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.0%;
41.9%;
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                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                            NCBI_TaxID=9913;
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P31888;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McKwam P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076343; AAH76343.1; -; mENA.
ZFIN; ZDB-GRNE-040718-173; zgc: 22.886.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA; 13957 MW; 9A9399E3683D7B16 CRC64;
                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| | || :|| :|| 83 NTATCVTHRLADFLSRSGGIGSSKFVPTNVGSQAF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                              126 AA.
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(Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001643; Amylin.
InterPro; IPR001643; Calcitonin-like.
InterPro; IPR001643; Calcitonin-like.
InterPro; IPR001643; Calcitonin B.
Pfan; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00814; CALCITONINB.
PRINTS; PR001848; ISLETAMYLOID.
SMART; SM00113; CALCITONIN; 1.
PROSITE; P800288; CALCITONIN; 1.
SEQUENCE 126 AA; 13957 MW; 9A9399B3
                                                              PRT;
                                                                                               25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, Zgc:92886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sednences.";
                                                        QEDGJ9 BRARE PRELIMINARY;
QEDGJ9;
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Best Local Similarity
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                                                                                                                                                                                     ORFNames=zgc:92886;
                                                                                                                                                                                                                                                                     Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA
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ID TAPP BOVIN

AC Q28207;

DT 15-JUL-1998 (

DT 15-JUL-1998 (
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                     RESULT 18
QEDGJ9_BRA
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13.62

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Gaps

9 NTATCVTHRLADFLSRSGGMGNSNFVPTNVGAKAF

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RESULT 22
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         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                     the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97057244; PubMed=8901583; DOI=10.1073/pnas.93.22.12344; Janaber H., Martial K., Zandberg J., Milhaud G., Benson A.A., Julienne A., Moukhtar M.S., Cressent M.; "Identification of a new calcitonin gene in the salmon Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel peptide 4 (Fragment).
Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal peptide.
calcitonin gene-related peptide 4.
carboxy terminal peptide.
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                                                                                                                                                                                                                                                        36.0%; Score 50; DB 1; Length 37; larity 37.1%; Pred. No. 0.057; Conservative 2; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cressent M.D.;
Submitted M.D.;
Submitted M.D.;
Submitted M.D.;
Submitted M.D.;
Submitted M.D.;
GD; GD: 171287; AAB38533.1; -; mRNA.
GO; GO: 0005576; C: extracellular region; IEA.
GO; GO: 0005179; F: hormone activity; IEA.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin-like.
Pfam; PF00214; Calc. CGRP_IAPP; T.
PRINTS; PR00817; CALCITONINB.
SMART; SM00113; CALCITONINB.
                                                                                                                                                                                                                By similarity.
OEFEE3AD2745EBDE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 93:12344-12348(1996)
                                                                                                                                                                                                    Phenylalanine amide.
                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00258; CALCITONIN; 1.
Amidation; Direct protein sequencing; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                             InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin B.
Pfam, PF00214; Calc_CGRP_IAPP; I.
PRINTS; PR00817; CALCITONINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5700 MW;
                                                                                                                                                                                                                              37 AA; 3887 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   P79814 ONCGO PRELIMINARY;
P79814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                       Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8017;
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SEQUENCE
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SEQUENCE
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                                                                       removed.
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Matches
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3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Metazoa, Chordata, Cramiata, Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Nooteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;

Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,

Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae, Takifugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and expression of Fugu calcitonin gene.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
R BMBL; AJ309015; CAC81277.1; -; Genomic DNA.
EMBEBL; AJ309015; CAC81277.1; -; Genomic DNA.
R Ensembl; SINFRUGO00125998; Fugu rubripes.
R GO; GO:0005576; C:extracellular region; IEA.
R InterPro; IPR000443; Amylin.
R InterPro; IPR000443; Amylin.
R InterPro; IPR002163; Calcitonin.B.
R FINTS; PR00214; Calc CGRP IARP; I.
R PRINTS; PR00819; CALCITONINB.
R PRINTS; R000113; CALCITONINB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 13 SCAF14769, whole genome shotgun sequence.
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||| || || :||
83 NTATCVTHRLADFLSRSGGMGNSNFVPTNVGAKAF 117
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                                                                         Created)
                                                                    01-JUN-2002 (TrEMBLrel. 21, Creat 01-JUN-2002 (TrEMBLrel. 21, Last 01-JUN-2003 (TrEMBLrel. 24, Last Calcitonin gene related peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00258; CALCITONIN; 1
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Q4S167;
                     FUGRU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31033;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Clark M.S.;
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FUGRU
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                   OBOFT9
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Moukhtar M.S.;
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Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.

GENOSCOPE, Whitehead Institute Centre for Genome Research;
Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Jansz H.S., Zandberg J.;
"Identification and partial characterization of the salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 49; DB 2; Length 184; 34.3%; Pred. No. 0.55; Live 3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.5%; Score 48; DB 2; Length 56; 34.3%; Pred. No. 0.22; cive 3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 AA; 20107 MW; 851FB9A69FD16F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcitonin/CGRP gene by polymerase chain reaction.";
Ann. N. Y. Acad. Sci. 657:63-69 (1992).
EMBL, S40497; AAB22593 1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000579; F:hormone activity; IEA.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR002163; Calcitonin-like.
PRINTS; PR00817; CaLCGRP IAPP; I.
PMRNTS; SM00817; CaLCGRP IAPP; I.
SMART; SM00113; CALCITONINB.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Calcitonin gene-related peptide (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 NTATCVTHRLADFLSRSGGMGNSNFVPTNVGAKAF 175
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CABEO1014769; CAGO5615.1; -; Genomic_DNA.
EMBL; CABEO1014769; LAGO5615.1; -; Genomic_DNA.
www.TER 184 184 184 184 184 189469FD16F25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q92164_ONCSP_PRELIMINARY;
Q92164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 34.3
Matches 12, Conservative
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Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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125 AA

PRT;

STANDARD;

CALCA CHICK P10286;

RESULT 25 CALCA CHICK ID CALCA CH AC P10286;

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and partial characterization of the calcitonin gene in a lower vertebrate. Predicted structure of avian calcitonin gene-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i-FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or
                            01-NOV-1991 (Rel. 7), Last sequence update)
10-MAY-2005 (Rel. 4), Last annotation update)
Calcitonin gene-related peptide precurdor (CGRP).
Name=CALCA, Synonyms=CALC;
Gallue gallue (Chicken).
Eukaryota; Metazoa; Chordata; Craniata/ Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evidence for the expression of a lower vertebrate calcitonin-like gene in man and rat.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 74-125.
MEDLINE-86248126; PubMed=3487468; DOI=10.1016/0014-5793(86)81425-9;
Minvielle S., Cressent M., Lasmoles F., Jullienne A., Milhaud G.,
                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE.
MEDLINE=88030046; PubMed=3666142; DOI=10.1016/0014-5793(87)80510-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Minvielle S., Cressent M., Delehaye M.C., Segond N., Milhaud Jullienne A., Moukhtar M.S., Lasmoles F.; "Sequence and expression of the chicken calcitonin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 12-73.
MEDLINE=86030240; PubMed=4054101;
Lasmoles F., Jullienne A., Day F., Minvielle S., Milhaud G.,
Moukhtar M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X06311; CAA29630.1; -; Genomic_DNA.
EMBL; X06312; -; NOT_ANNOTATED_CDS; Genomic_DNA.
EMBL; X06312; -; NOT_ANNOTATED_CDS; Genomic_DNA.
EMBL; X063012; CAA26796.1; ALT_TERN; mRNA.
EMBL; D00007; BAA00006.1; -; Genomic_DNA.
EMBL; S001057; TCCHRP.
EIR; $00107; TCCHRP.
EIR; $00107; EXSCALGO0000006054; Gallus gallus.
InterPro; IPR001043; Amylin.
InterPro; IPR001043; Amylin.
InterPro; IPR001043; Calcitonin_like.
InterPro; IPR001043; Calcitonin_B.
Pfam; PF00214; Calc.GGRP_IAPP; I.
PRINTS; PR00811; CALCITONINB.
PRINTS; PR00811; CALCITONINB.
SWART; SM00113; CALCITONIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuromodulator role.
SUBCELLULAR LOCATION: Secreted.
ALTENRALTIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=Calcitonin-gene related peptide;
IsoId=P10286-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P07660-i, Sequence=External;
-!- SIMILARITY: Belongs to the calcitodin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lett. 203:7-10(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. 4:2603-2607(1985)
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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NUCLEOTIDE SEQUENCE.
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HERE REPORTED TO THE PROPERTY OF THE PROPERTY 
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                                      Phenylalanine amide (G-117 provides amide
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein (Fragment).
ORFNames-CaO19.1346, CaO19.8926;
Candida albicans SC5314.
Eukaryota; Fungi; Aecomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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0
  Calcitonin gene-related peptide
                                                                                                                                                  Score 48; DB 1; Length 125;
Pred. No. 0.56;
2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2; Length 25; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Dijk M.A.;
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL286813; GAC28526.1; Genomic_DNA.
GG; GG:0005179; F:hormone activity; IEA.
InterPro; IPR001643; Amylin.
InterPro; IPR001693; Calcitonin-like.
FEGN; PF00214; Calc CGRP IAPP; 1.
PRINTS; PR00818; ISLETANYLOID.
SMART; SM00113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van Dijk M.A.M., de Jong W.W.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                        group).

By similarity.

D -> E (in Ref. 2).

EB64A2C9AC111F80 CRC64;
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25 AA; 2723 MW; 911B2C02FB677BAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                        82 NTATCVTHRLADFLSRSGGVGKNNFVPTNVGSKAF 116
                                                                                                                                                                                                                                 3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TQRLXNFLXXXXXXXXGPXLPXTXVG 33
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                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
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Islet amyloid polypeptide (Fragment)
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                                                                                                                 13729 MW;
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44.0%;
                                                                                                                                                      34.5%;
37.1%;
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                                                                                                                                 Query Match
Query Match
Best Local Similarity 37....
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 44.v.
Best Local 11, Conservative
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Q59PMS;
                                                                                                                                                                                                                                                                                                                                                                     Q9BEE1 MACRU PRELIMINARY,
Q9BEE1;
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56
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                                                                                                                 125 AA;
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56
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    PEPTIDE
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1D QS
AC QS
AC QS
DT 10
DT 10
DD HY
OS Ca
  SHEFFE
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthonard V., Jubin C., Castellia G., Dossat C.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutenceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Buteleostomi;

Schinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., bungan J., Kalman S.,
Jagee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
                                                                                                                                                                                                                                                                                                                                    Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Onones T., Scherer S., Agabian N.; "Amnotation of the Genome of Candida albicans."; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FB-2004) to the EMEL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; CAAEDIO14881; CAP99659.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.7%; Score 45.5; DB 2; Length 560; 31.0%; Pred. No. 9.4; cive 2; Mismatches 12; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 AA; 57345 MW; 3E43DB925417CB14 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 5 SCAF14581, whole genome shotgun sequence.
                                                                                                                                                  "The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AACQ01000188; EAK92446.1; -; Genomic_DNA. EMBL; AACQ01000187; EAK92464.1; -; Genomic_DNA.
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Best Local Similarity 31.09
Matches 13, Conservative
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ID Q4SI73 TETNG PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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CALCA PIG
P30880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peck B., Ortkamp O., Diehl K.D., Knapp B.;
"Molecular cloning, conservation, localization and expression of HopZ, an outer membrane protein of Helicobacter pylori.";
Nucleic Acids Res. 27:3325-3333(1999).
EMBL: Y18991; CAB42979.1; -; Genomic_DNA.
                                                                                                                                          Gaps
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Mammalia, Eutheria, Euarchontoglires, Glires, Lagomorpha, Leporidae,
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Helicobacteraceae; Helicobacter.
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                                                                               DB 2; Length 51;
                                                                                                                                    20; Indels
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26E1E7F612DEB90D CRC64;
                          45D08BE150FC9FEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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(Rel. 36, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                                                                               667 AA.
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                                                                               Score 45; DB 2; Pred. No. 0.78; 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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72688 MW;
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Pfam; PF01856; HP OMP; T.
PRINTS; PR01776; HPOMPFAMILY.
                                                                                  32.4%;
  51
5551 MW;
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                                                                               Query Match 32.4
Best Local Similarity 34.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Q9X748_HELPY PRELIMINARY;
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51 AA;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration
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FUNCTION: Selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism.

SUBCELDULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from porcine spinal cord.";
Neuropetides 9:75-82(1987).
-!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
vessels including the coronary, cerebral and systemic vasculature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimura S., Sugita Y., Kanazawa I., Saito A., Goto K.; "Isolation and amino acid sequence of dalcitonin gene related peptide
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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By similarity.
04CDEB8D248B64BA CRC64;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the calcitonin family.

    -!- SIMILARITY: Belongs to the calcitodin family.

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01-UU-1993 (Rel. 26, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Calcitonin gene-related peptide (CGRP).
Sus scrofa (Pig).
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SMART; SM00113; CALCITONIN; 1.
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PIR; 146933; 146933.
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56.2%;
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nes 9; Conservative
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Callithrix jacchus (Common marmoset)
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A SERVICE SERV
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Arthouard V., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., volff JN., Guigo R., Zody M.C., Mešrov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames-GSTENGO000464001;
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei, Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopperygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF2800, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 1.6;
1; Mismatches 4; Indels
                                DB 1; Length 37;
1.3;
                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AA; 4556 MW; EE24C0ED223F4E96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                       37
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                                                                                                                                                       3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                              44 AA.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-UDN-2003 (TrEMBLrel. 24, Last annotation
Beta-calcitonin-related protein (Fragment).
                                Score 43; DB Pred. No. 1.3; 1; Mismatches
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                                34.3%;
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Best Local Similarity 64...
9; Conservative
         Query Match
Best Local Similarity 34.3
                                                                                                                                                                                                                                                                                                                                                                        Q4THN9_TETNG PRELIMINARY;
Q4THN9;
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QBWNX2;
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NUCLEOTIDE SEQUENCE.
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Q8WNX2 CAI
ID Q8WNX
AC Q8WNX
DT 01-MP
DT 01-MP
DT 01-MP
DE BETA-
GN NAME=
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nowno apprens (menazo) (hordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazo; Chordata; Craniata; Primates; Catarrhini; Hominidae;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=87109142; PubMed=3492492;
Petermann J.B., Born M., Chang J.Y., Fischer J.A.;
"Identification in the human central nervous system, pituitary, and thyroid of a novel calcitonin gene-related peptide, and partial amino acid sequence in the spinal cord.";
J. Biol. Chem. 262:542-545(1987).
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MEDLINE-85180007; PubMed=2985435; DOI=10.1016/0014-5793(85)80820-6;
Steenbergh P.H., Hoeppener J.W.M., Zandberg J., Lips C.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87105923; PubMed=3492393; DOI=10.1016/0014-5793(86)81091-2; Steenbergh P.H., Hoeppener J.W.M., Zandberg J., Visser A., Lips C.J.M., Jansz H.S.;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Platyrrhini,
Callitrichidae, Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P1009<u>7</u>; Q9UCN9;
01-MAR-1989 (Rel. 10, Created)
10-MAR-1989 (Rel. 10, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation ubdate)
Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Siructure and expression of the human calcitonin/CGRP genes."; PBBS Lett. 209:97-103(1986).
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                                                                                                                                                                                                    Schindler M., Fischer E.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF42154; AAL35593.1; -; Genomic DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin B.
Pfam; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00817; CALCITONINB.
SMART; SM00113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.9%; Score 43; DB 2; Length 53; 34.3%; Pred. No. 2;
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"A second human calcitonin/CGRP gene.";
FRBS Lett. 183:403-407(1985).
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MEDLINE-90211348; PubMed=2322288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12, Conservative
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                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                            NCBI_TaxID=9483;
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                  Homo sapiens (Human)
                                                                                                                                             [1]
NUCLEOTIDE SEQUENCE.
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                                                                                                                       NCBI_TaxID=9606;
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Q99MP3;
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Local Sim
12;
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 셤
                                                                                                                                                                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                          "Isolation, purification and characterization of beta-hCGRP from human spinal cord.";
                                                                                                                     Phenylalanine amide (G-119 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
 Wimalawansa S.J., Morris H.R., Etienne A., Blench I., Panico M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcitonin gene-related peptide II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC; HGNC: HGNC: HGNC: HGNC; HGNC; HGNC; HGNC: 
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                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the calcitonin family.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X04855; CAC05295.1; -; Genomic_DNA.
EMBL; X04857; CAC05295.1; JOINED; Genomic_DNA.
EMBL; X04861; CAC05295.1; JOINED; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSG0000175868; Homo sapiens
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
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PIR; A25864; A25864.
PIR; 137232; 137232.
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                                                                                                      PROTEIN SEQUENCE OF 82-104.
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Q56910;
10-MAY-2005 (TrEMBLrel 3(
10-MAY-2005 (TrEMBLrel) 3(
                                                                                                                                                                                                                                                                                       neuromodulator role.
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nes 12; Conserv
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1D 056
AC 056
DT 10
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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PS FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BC092468; AAH92468; AH92468; BRNAA.
Ensembl; ENSG00000175868; Home sapiens.
GO, GO:0005576; C:extracellular region; IEA.
GO; GO:0005179; F:hormone activity; IEA.
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INTERPRO; IPRO00443; Amylin.
INTERPRO; IPRO01693; Calcitonin-like.
INTERPRO; IPRO0163; Calcitonin B.
Fam; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00118; ISLETANYLOID.
SWART; SM00119; CALCITONIN; I.
PROSITE; PR00258; CALCITONIN; I.
SEQUENCE 127 AA; 13706 MW; B0A7IA063CD5ACE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 NTATCVTHRLAGLLSRSGGMVKSNFVPTNVGSKAF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%; Score 43; DB 2; ilarity 34.3%; Pred. No. 5.4; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA.
Calcitonin-related polypeptide, beta.
Name=CALCB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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'Genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPBIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPBIAS
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                                                                                                                                                                                                                                            removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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ID DTT DDT TD DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
Calcitonin gene-related peptide II.
By similarity.
Phenylalanine amide (G-121 provides amide group) (By similarity).
By similarity.
                                                                                                                                                      alpha and beta genes.";

DNA Seq. 12:131-135 (2001).

-!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role (By similarity).

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                               STRAIN=129/Sv;
MEDLINE=21604266; PubMed=11761712;
Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;
"Structure of the mouse calcitonin/calcitonin gene-related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage on pair of basic residues; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1; Length 130;
Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97299244E8F6C536 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF325526; AAK16431.1; -; Genomic DNA.
EMBL; AF325524; AAK16431.1; JOINED; Genomic DNA.
ENSEMD1; ENSMUSGO000030666; Mus musculus.
MGI; MGI:2151254; Calcb.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000443; Amylin.
InterPro; IPR00143; Amylin.
InterPro; IPR00143; Alcitonin-like.
InterPro; IPR001163; Calcitonin B.
PRINTS; PR008117; CALCITONINB.
PRINTS; PR008119; CALCITONINB.
SMART; SM00113; CALCITONIN, 1.
PROSITE; PS00258; CALCITONIN, 1.
                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the calcitonin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 15, Created)
28-FRB-2003 (Rel. 11, Last sequence update)
Hypothetical protein C30G12.1 in chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The C. elegans sequencing consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 90 E
130 AA; 14623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9%;
34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 12; Conserv
                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=C30G12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
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Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
Arroya J., Beriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Arroya J., Beriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Arroya J., Beriman M., Coulsen R., Davies R., Dyer P.S.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Reman M., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
Rosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Reller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
Rumagai T., Lafton A., Latge J.-P., Lil W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Mond M.,
Anjoros W.H., May G.S., Miller B.L., O'Neil S., Paulsen I.., Quail M.A.,
Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
Ronning C.M., Rutter S., Salzberg S.L., Sanchez M., Squares S.,
Takeuchi M., Tekaia P., Turner G., Vazquez de Aldana C.R., Weidman J.,
White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
Anchida M., Hall N., Barrell B., Denning D.W.,
Genomic sequence of the pathogenic and allergenic filamentous fungus
                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi; Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
                                                                                                                                                                              WormBase consortium; Submitted (OCT-2001) to the EMBL/GenBan\mathbf{k}/\mathrm{DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           845099206BB9885D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequente update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 NVATTTTPLPLRFILPTPAAPNPFLPSTRVG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, U21319; AAL16307.1; -; Genomic DNA. Bnsembl; C30G12.1; Caenorhabditis elegans. Wormbase; WBGene00016273; C30G12.1. CE29685. Interpro; IPR010480; Prot inh I33. Pfam; PP06394; Pepsin-I3; I. Complete proteome; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly-Thr.
Poly-Thr.
Poly-Ser.
Poly-Thr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52847 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus Af293.
                                       investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q4WLC6 ASPFU PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=Afu6g14020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=330879;
                                                                                                                                      SEQUENCE REVISION
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SEQUENCE [LARGE SCALE GENOMIC DNA].

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Loftus B.J., Fung E., Roncagina P., Rowley D., Amedeo P., Bruno D., Amathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet II.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., Dosdara C.A., Fox D.S., Grinberg V., Fu J., Friushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G. Pertea M., Riggs F.R., Salzberg S.L., Schain J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W.;

T. The genome of the basidiomycetous yeast and human pathogen C.Typtococcus neoformans.";

C.Typtococcus neoformans.";

Science 307:1321-1334(2005).

R. EMBL, AE017353; AAW46737.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
30.9%; Score 43; DB 2; Length 1502;
Best Local Similarity 33.3%; Pred. No. 89;
Matches 11; Conservative 2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 1502 AA; 164198 MW; AEF63A266216FF3C CRC64;
                                                                                                       PubMed=15653466; DOI=10.1126/science.1103773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     removed.
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Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Aspergillus fumigatus.";
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=B-3501A;
Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ entry which is
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                                                                                                                                                                                                                                                                                                    Score 43, DB 2; Length 482;
Pred. No. 25;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%; Score 43; DB 2; Length 150
33.3%; Pred. No. 89;
tive 2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.

EMBL, AREYO1000064; EAL17429.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 1502 AA; 164196 WW, AEF63A266216FF3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 482 AA; 53183 MW; BE79BD9B597F8216 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
Translational initiation-related protein, putative.
OKENAMES-CNM02490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                      preliminary data.
EMBL; AAHF01000006; EAL89238.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               956 TATDAVSHFLNCLLGSCLNPAPVASYTPIGINS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cryptococcus neoformans var. neoformans JEC21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                    30.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 GPEIPYTIYGSNSF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q55HY4_CRYNE PRELIMINARY;
Q55HY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSK7G8 CRYNE PRELIMINARY;
QSK7G8;
                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
ORFNames=CNBM2330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                       Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothalamic extract.";
Biochem. Biophys. Res. Commun. 187:1474-1479(1992).
-!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
vessels including the coronary, cerebral and systemic vasculature.
Its abundance in the CNS also points toward a neurotransmitter or
                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2015 (Rel. 47, Last annotation update)
Name-CALCA: Synonyms-CALC;
Ovis axies (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Hypothalamus;
MEDLINE=93038624; PubMed=1417824;
Miyata A., Jiang L., Minamino N., Arimura A.;
"Identification of calcitonin gene related peptide in ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Its abundantor role.
-!- SUMILARITY: Belongs to the calcitonin family.
-!- SIMILARITY: Belongs to the calcitonin family.
                                  956 TATDAVSHFLNCLLGSCLNPAPVASYTPIGINS 988
4 TATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JH0709; JH0709.

InterPro; IPR001693; Calcitonin-like.

InterPro; IPR002163; Calcitonin B.

Pfam; PF00214; Calc CGRP IAPP; I.

PRINTS; PR00817; CALCITONINB.

SMART; SM00113; CALCITONIN; 1.
                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                CALCA SHEEP
P30881;
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NUCLEOTIDE SEQUENCE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Bammalia, Eutheria, Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae, Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type
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Martinez-Millan L.;
                                                                                                                                                             30.2%; Score 42; DB 1; Length 37; 34.3%; Pred. No. 2.1; ive 1; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.2%; Score 42; DB 2; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Indels
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                                                                                                          FSDDF64D248B6A47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Alpha-calcitonin gene-related peptide (Fragment)
                                                        Phenylalanine amide.
                                                                                                                                                                                                                                                                       3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                          3 NTATCVTHRLAGLLSRSGGVVKSNFVPTNVGSQAF 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                 Hormone
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                                                                                    By similarity
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                            Amidation; Direct protein sequencing; MOD RES 37 Phenylala DISŪLFID 2 7 By simila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
  PROSITE; PS00258; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00258; CALCITONIN; 1
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                                                                                                             37 AA; 3780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                        12; Conservative
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                                                                                                                                                                                              Local Similarity
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                                                                                                                SEQUENCE
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IsoId=P01257-1; Sequence=External;
-!- SIMILARITY: Belongs to the calcitonin family.
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                                                                                                                                                                                                                                                                                                                                                                   84
40
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128 AA;
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09N0T3;
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Calcitonin gene-related peptide I.
By similarity.
Phenylalanine amide (G-120 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CREP induces vasodilatation. It dilates a variety of vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role.

SUBCELLULAR LOCATION: Secreted.

ALTERNATIVE PRODUCTS:

Revent-Alternative splicing; Named isoforms=2;
Name-Calcitonin-gene related peptide I;
IsoId=P01256-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE-81300490; PubMed=2994212;
Amara S.G., Arriza J.L., Leff S.E., Swanson L.W., Evans R.M.,
Rosenfeld M.G.;
"Expression in brain of a messenger RNA encoding a novel neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                         Gaps
                                SMART; SM00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
Alternative splicing; Amidation; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE 82220111; PubMed=6283379; Amara S.G., Jonas V., Rosenfeld M.G., Ong E.S., Evans R.M.; Amara S.G., Jonas V., Rosenfeld M.G., Ong E.S., Evans R.M.; Alternative RNA processing in calcitonin gene expression generates mRNAs encoding different polypeptide products.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85166259; PubMed=1872459; Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W., Jonas V., Lin C.R., Rosenfeld M.G.; Mermod J.-J., Evans R.M., Rosenfeld M.G.; Alternative RNA processing events in human calcitonin/calcitonin gene-related peptide gene expression."; Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).
                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-ARY-1988 (Rel. 07, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type
                                                                                                                                                                                                         ;;
0
                                                                                                                                                                                 Score 42; DB 1; Length 128;
Pred. No. 8.6;
                                                                                                                                                                                                         22; Indels
                                                                                                                                     group).

By similarity.

83BB0E36C8B4239E CRC64;
                                                                                                                                                                                                                                                    85 NTATCVTHRLAGLLSRSGGVVKDNFVPTNVGSEAF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homologous to calcitonin gene-related peptide."; Science 229:1094-1097(1985).
                                                                                                                                                                                                                             3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                             128 AA
                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                             PRT;
Pfam; PF00214; Calc CGRP IAPP; 1.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
                                                                                                                                               84 89 B
128 AA; 14065 MW;
                                                                                                                                                                                34.3%;
                                                                                                                                                                                                                                                                                                                                                                                           Name=Calca; Synonyms=Calc;
                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
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119
128
119
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                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                        26
83
125
119
                                                                   Hormone; Signal
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                                                                                       PROPEP
PRPTIDE
PROPEP
MOD_RES
                                                                                                                                                            SEQUENCE
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                                                                               SIGNAL
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinfórmatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Alternative splicing; Amidation; Cleavage on pair of basic residues; Hormone; Signal.
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Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
SPERB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last amotation update)
Calcitonin gene-related peptide II predursor (CGRP-II) (Beta-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcitonin gene-related peptide I.
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Pred. No. 8.6;
1; Mismatches 22; Indels
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By similarity.

Missing (in Ref. 2 and 3).

Missing (in Ref. 2 and 3).

Q -> EEQ (in Ref. 2 and 3).

S -> R (in Ref. 3).
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                                                                                                                                                                                                                                                                                                           EMBL; L29188; AAB59682.1; -; Genomic_DNA.
EMBL; L001109; AAB59682.1; JOINED; Genomic_DNA.
EMBL; L00110; AAB59682.1; JOINED; Genomic_DNA.
EMBL; V01221; CAAZ4541.1; -; mRNA.
EMBL; M11597; AAA40847.1; -; mRNA.
PIR; A01524; CTRTR.
PIR; B44173; B44473.
InterPro; IPR001493; Amylin.
InterPro; IPR001493; Calcitonin-like.
InterPro; IPR001693; Calcitonin-like.
PFOM214; Calc CGRP IAPP; IPR01214; Calcitonin B.
PRINTS; PR00818; ISLETAMYLOID.
PRINTS; PR00818; ISLETAMYLOID.
SMART; SM0113; CALCITONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 NTATCVTHRLAGLLSRSGGVVKDNFVPTNVGSEAF 119
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                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
A Att-zahra M., Allen N., Allen T., An P., Baderson S.,
A Arachchi H., Armbruster J., Beloam T., Blye J., Boguslavskiy L.,
Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
Bayul T., Gamzata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
Calvos S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
Callymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
David R., Dawce T., Degray S., Dodges S., Dooley K., Doris P.,
Dorise K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
Erickson J., Farina A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,
Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
Lindbladtetoh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
Lindbladtetoh K., Liu X., Lokyitsang T., Lokyitsang C., Major J.,
Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
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By similarity.

Calcitonin gene-related peptide II.

By similarity.

Phenylalanine amide (G-121 provides amide
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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By similarity.
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Last annotation update)
                             SIMILARITY: Belongs to the calcitonin family.
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1; Mismatches
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InterPro; IPR000443; Amylin.
InterPro; IPR001693; Calcitonin-like.
InterPro; IPR001693; Calcitonin B.
Pfan; PF00214; Calc CGRP IAPP; I.
PRINTS; PR00817; CALCITONINB.
PRINTS; PR00818; ISLETAMYLOID.
SWART; SW00113; CALCITONIN; 1.
PROSITE; PS00258; CALCITONIN; 1.
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   SUBCELLULAR LOCATION: Secreted
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129 AA; 13925 MW;
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QSIQAI;
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Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
Mozes J., Mihaler L., Munnson G., Naylor J., Newes C., Nguyen C.,
Myuyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
Myuyen N., Osman S., Parker S., Perrin D., Phukhhang P., Piqani B.,
O'neill K., Osman S., Parker S., Perrin D., Phukhhang P., Piqani B.,
Purcell S., Rachupka T., Ramsaway U., Ramsawa R., Ray V., Raymond C.,
Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
Spencer B., Stalker J., Stenge-thomann N., Stavropoulos S.,
Stetson K., Stone S., Theodore J., Thoulutsang Y., Tchuinga P.,
Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Tchuinga P.,
Vorketaraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
Wang S., Yang X., Yanger S., Yee E., Young G., Zainoun J., Zembeck L.,
M. Zimmer A., Zody M., Lander E.;
M. Minh, Canner B.,
M. Manger E.,
M. Minh, Canner E.,
M. M., Manger E.,
M. Minh, Canner E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AACUO1001389; EAA48567.1; -; Genomic DNA.
SEQUENCE 171 AA; 18327 MW; FF892C245B62E04E CRC64;
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Bukaryota; Perizomycotina; Sordariomycetes;
Hypocreomycetidae, Hypocreales; Nectriaceae; Gibberella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.2%; Score 42; DB 2; Length 171; 22.9%; Pred. No. 12;
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Dean R., Mitchell T., Brown D., Pan H., Thon M.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Magnaporthe grisea."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequente update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 AA.
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Best Local Similarity 22.9°
Matches 8; Conservative
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ORFNames=FG09000.1;
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NUCLEOTIDE SEQUENCE.
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MUCLECOTIDE SEQUENCE.

MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holt R.A., Floskins R.A., Galle R.F.,
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Sutton G.G., Worman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
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Berkova D., Botchan M.R., Bouck J., Brokstein P., Botter P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Abris K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
Abrohn K.J., Evangelista C.C., Ferraz C., Rerriera S., Fleischmann W.,
Podson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Rerriera S., Fleischmann M.,
Rolodek A., Gong F., Gorrell J.H., Gu Z., Ghan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Soman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S. Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Tralamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M. Lander E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Park S., Sequeira S.R., Kim E., Li P., Moshrefi M., Pacleb J.M. Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.,
                                                                                                                                                                                                                                                                                                                                                    "Pusarium graminearum genome sequence.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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09Y0234

01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
110-MAY-2005 (TrEMBLrel. 30, Last annotation update)
110-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.2%; Score 42; DB 2; Length 378; 39.4%; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 378 AA; 41574 MW; AlDF6COC66E0650C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
; AACM01000367; EAA77358.1; -; Genomic_DNA.
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C9Y029 DROME
DAC 09Y029; DD
DT 01-NOV-1; DD
DT 01-NO
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Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke £., Kennison J.A., Ketchum K.A.,
Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Lei Y., Lei Y., Li J.H., Li Z., Liang Y., Lin X.,
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Liu X., Mattei B., McIntosh T.C., McLeod M. P., McPherson D. L.,
Mount S.M., Moy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuiskern D.R., Pacleb J.M.,
Reinert K., Remington K., Saunders R.Dic., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun K.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Milliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. Hilliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. Cheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Feiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finlahing a Wold-genome shotgun: relafase 3 of the Drosophila melanogaster euchromatic genome sequence.", George Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grøy A.D.N.J., Drygdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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EMBL; AE003660; AAN11018.1; -; Genomic_DNA.
HSSP; P50480; 1BWS.
SMR; Q9Y0Z9; 240-304.
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DROME
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Q9VJ37_DRO
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MEDLINE=97234720; PubMed=9115734; DOI=10.1016/S0896-6273(00)81241-6;
Thor S., Thomas J.B.;
Thor S., Thomas J.B.;
The Droscophila islet gene governs axon pathfinding and
neurotransmitter identity.";
Neuron 18:397-409[1997].
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
EMBL; U89385; AAB49892.1; -; mRNA.
HSSP; P50480; 1885.
SRR; P92031; 240-304.
FlyBase; FBgn0003896; tup.
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Name=tup; Synonyms=islet; ORFNames=CG10619;

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neopiera; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
R GO; GO:00046665; P:amnioserosa maintenance; IMP.
R GO; GO:0007391; P:dorsal closure; TAS.
R GO; GO:0007391; P:dorsal closure; TAS.
R GO; GO:0007399; P:neurogenesis; TAS.
R GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
R GO; GO:000293; P:rorso signaling pathway; IGI.
R GO; GO:000293; P:rorso signaling pathway; IGI.
R InterPro; IPR012287; Homeodox.
InterPro; IPR001707; LIM homeo.
InterPro; IPR001707; LIM homeo.
InterPro; IPR001707; LIM, 2.
R Pfam; PF00412; LIM, 2.
R PFMINTS; PR00024; HOMEOBOX.
R RSWART; SM00132; LIM, 2.
R RNART; SM00139; HOMEOBOX.
R R RROSITE; PS00017; HOMEOBOX.
R R ROSITE; PS00017; HOMEOBOX.
R R ROSITE; PS00017; HOMEOBOX.
R PROSITE; PS00013; LIM DOMAIN.
R PROSITE; PS000
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GO:0007391; P:dorsal closure; TAS.
GO:0007390; P:germ-band shortening; IMP.
GO:0007399; P:neurogenesis; TAS.
GO:0007362; P:terminal region determination; IGI.
GO:0008293; P:torso signaling pathway; IGI.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GO; GO:0008258; P:head involution; NA
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007362; P:terminal region det
GO; GO:000829; P:terminal region det
InterPro; IPRO1356; Homeobox.
InterPro; IPRO1356; Homeobomain-rel.
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InterPro; IPR001781; LIM_Zn_bd.
Pfam; PF00046; Homeobox; 1.
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RECORDING SEGUENCE.

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.C., Scherer S.E., It P.W., Hoskins R.A., Galle R.F.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Abril J.F., Agabayani A., An H.-J., Andrews-Ptennatoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktarcglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktarcglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktarcglu L., Beasley E.M.,

Ballew R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Bartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Charter P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Dunn P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Dunn P.,

Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,

Bockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Borlor C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

Harris N.L., Harvey D.A., Heiman T.J., Herrandez J.R., Hock T.,

RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Melson D.R., Nelson K.A., Nowland T.J., Wei M.-H., Ibegwam C.,

Rako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lan X.,

Melson D.R., Nelson K.A., Nixon K., Norskern D.R., Packer M.G.,

Reinert K., Remington K., Saunders R., Warty D.M., Nelson D.L.,

Rander B.C., Schen Kiamos I., Simpson M., Suppski M.P., Smith T.,

Spier B., Spradling A.C., Stapleton M., Strong R., Supski M.P., Smith Y.,

Spier B., Spradling A.C., Stapleton M., Strong R., Weissenbach J.,

RAN Hanges B.M., Wooder T., Worley K.C., Wu D., Yang S., Yao, A.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wei
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophilidae; Drosophila.
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                                                                                                PROSITE; PS00027; HOMEOBOX_1; UNKNOWN_1.
PROSITE; PS00071; HOMEOBOX_2; 1.
PROSITE; PS00073; LIM_DOMAÏN_1; 2.
PROSITE; PS000478; LIM_DOMAÏN_1; 2.
DNA-binding; Developmental protein; Homeobox; LIM domain; Metal-binding; Nuclear protein; Transcription;
Transcription regulation; Zinc.
SEQUENCE 534 AA; 58055 MW; 86FDC47639B6D7C3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2004 (TrEMBLrel. 26, Last annotation update)
CG10619-PA, isoform A.
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Pfam; PF00412; LIM; 2.
PRINTS; PR00024; HOMEOBOX.
SMART; SM0389; HOX; 1.
SMART; SM0132; LIM; 2.
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Search completed: January 4, 2006, 11:45:36
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MEDLINE=2242605; PubMed=12537568;
MEDLINE=2242605; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe W., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Peiffer B.D., Richards S., Sodergren B.J., Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinschock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
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MEDLINE=22446070; PubMed=12537573;
MEDLINE=22446070; PubMed=12537573;
Kaminker JS., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195 (2000).
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MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drygdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
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"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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GO; GO:0046665; P:amnioserosa maintenance; IMP.
GO; GO:0007391; P:dorsal closure; TAS.
GO; GO:0007390; P:germ-band shortening; IMP.
GO; GO:0007390; P:serm-band shortening; IMP.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0007389; P:terminal region determination; IGI.
GO; GO:00073823; P:torso signaling pathway; IGI.
InterPro; IPR011386; Homeobox.
InterPro; IPR011287; Fur Homeodomain-rel.
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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42.3%; Pred. No. 43;
vative 2; Mismatches
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PROSITE; PS50017; HOMEOBOX_2; 1.
PROSITE; PS00478; LIM DOMAIN 1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
InterPro; IPR001781; LIM Zn bd.
              Pfam; PF00046; Homeobox; 1.
Pfam; PF00412; LIM; 2.
                                           PRINTS; PR00024; HOMEOBOX.
SMART; SM00389; HOX; 1.
SMART; SM00132; LIM; 2.
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371 NTHTPAFQQLVNQMHGYDLNGMPILP 396

3 NTATXATQRLXNFLXXXXXXXXGPXLP 28

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1 XXNTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                      GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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A;Reference number: S05037; MUID:89325677; PMID:2666169
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                                A; Residues: 38-74 < BET>
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A; Residues: 1-93 <VAN>
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NiAlternate names: insulinoma amyloid protein
C;Species: Mus musculum (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C33542; S05039
R;NiBhi, M; Chan, S.1.; Nagamatsu, S.; Bell, G.I.; Steiner, D.F.
R;NiBhi, M; Chan, S.J.; Nagamatsu, S.; Bell, G.I.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 5738-5742, 1989
A;Title: Conservation of the sequence of islet amyloid polypeptide in five mammals is cc
A;Reference number: A33542; MUD:89345542; PMID:2668946
A;Accession: C33542
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <NIS
A;Residues: 1-93 <NIS
A;Residues: 1-93 <NIS
A;Residues: 1-93 <NIS
A;Residues: UNIPROT:P12968; UNIPARC:UPI000001A43; GB:M25389; NID:g194066; PIDN:
A;Note: the authors translated the codon CTG for residue 18 as Ser, and CTC for residue
R;Betsholtz, C.; Christmansson, L.; Engstroem, U.; Rorsman, F.; Svensson, V.; Johnson, R;Rests Lett. 251, 261-264, 1989
A;Title: Sequence divergence in a specific region of islet amyloid polypeptide (IAPP) ex
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NyAlternate names: amylin precursor, diabetes-associated peptide; insulinoma amyloid prote; Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: 813566; A30312; B33542; A33426; S05038; A35481; B35481 J. Ps.
R;van Mansfeld, A.D.M.; Mosselman, S.; Hooppener, J.W.M.; Zandberg, J.; van Teeffelen, H Biochim. Biophys. Acta 1087, 235-240, 1990
A;Title: Islet amyloid polypeptide: structure and upstream sequences of the IAPP gene in A;Reference number: S13566; MUID:91027936; PMID:2223885
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A; Title: Rat amylin: cloning and tissue-specific expression in pancreatic islets. A; Reference number: A30312; MUID: 89240689; PMID: 2654937
A; Accession: A30312
A; Residues: 1-93 < LEF>
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Proc. Natl. Acad. Sci. U.S.A. 86, 5738-5742, 1989
A;Title: Conservation of the sequence of islet amyloid polypeptide in five mammals is con A;Reference number: A33542; MUID:89345542; PMID:2668946
A;Recession: B33542
A;Molecule type: mRNA
A;Residues: 1-33 <NIS>
A;Molecule type: mRNA
A;Residues: 1-31 <NIS>
A;Cross-references: UNIPARC:UPI000012D0CA; GB:M25390; NID:g204676; PIDN:AAA41359.1; PID:gN:ABai, J; Nakazato, M.; Kangawa, K.; Matsukura, S.; Matsuo, H.
Biochem: Biophys. Res. Commun. 144, 400-405, 1989
A;Ttle: Isolation and sequence determination of rat islet amyloid polypeptide.
A;Reference number: A33426; MUID:90026410; PMID:2679555
A;Accession: A3426.
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A; Residues: 38-74 <ASA>
A; Residues: 38-74 <ASA>
A; Cross-references: Univaristic to the content of the content of
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Biochem. Biophys. Res. Commun. 169, 788-795, 1990
A,Title: Regional distribution and molecular forms of rat islet amyloid polypeptide.
A,Reference number: A35481; MUID:90290528; PMID:2357234
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A; Accession: S05039
A; Status: not compared with conceptual translation A; Molecule type: mRNA
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A;Residues: 38-74 <BET>
A;Cross-references: UNIPARC:UP1000003519C
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C;Superfamily: calcitonin
C;Keywords: amyloid
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A; Cross-references: UNIPARC: UPI000016AAD6
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A; Molecule type: mRNA
A; Residues: 1-92 <NIS>
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A;Cross-references: UNIPARC:UPI000003519C
A;Accession: B35481
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A;Cross-references: UNIPARC:UPI000003519C
A;Cross-references: UNIPARC:UPI000003519C
A;Cross-references: UniPARC:UPI000003519C
C;Keywords: amidated carboxyl end; amyloid; pancreatic islet
C;Keywords: amidated carboxyl end; amyloid; pancreatic islet
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-37/Domain: signal sequence #status predicted <SIG>F;24-37/Domain: amino-terminal propeptide #status predicted <PROI>F;38-74/Product: insulinoma amyloid protein #status experimental <AMT>F;38-37/Domain: carboxyl-terminal propeptide #status predicted <PROI>F;39-44/Disulfide bonds: #status predicted
F;74-Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
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(Species: Octobon degus (degu)
(C,Species: Octobon degus (degu)
(C,Species: Octobon degus (degu)
(C,Species: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
(C,Accession: A36118
R,Nishi, M.; Steiner, D.F.
R,Nishi, M.; Steiner, D.F.
R,Nishi, M.; Steiner, D.F.
A,Reference number: A36118; MUD: 91155952; PMID: 2293024
A,Reference number: A36118
A,Reference number: A36118
A,Residue: preliminary
A,Molecule type: mRNA
A,Residue: 1-91 kNIS.
A,Residue: 1-91 kNIS.
C,Superfamily: calcitonin
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C;Date: 07-sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S05037
R;Betsholtz, C.; Christmansson, L.; Engstroem, U.; Rorsman, F.; Svensson, V.; Johnson, FEBS Lett. 251, 261-264, 1989
A;Title: Sequence divergence in a specific region of islet amyloid polypeptide (IAPP) e A;Reference number: S05037; MUID:89325677; PMID:2666169
A;Reference number: S05037
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Pred. No. 1.9e-14;
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C;Superfamily: calcitonin
C;Keywords: amyloid
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Pred. No. 7.4e-16;
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Pred. No. 1.7e-14;
0; Mismatches 12;
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68.6%;
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65.7%;
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Best Local Similarity 68.57
Thos 24; Conservative
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Matches 23; Conservative
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islet amyloid polypeptide precursor (validated) - human N;Alternate names: amylin precursor; diabetès-associated peptide; insulinoma amyloid pro C;Species: Homo sapiens (man) C;Dates: 31-Mar-1993 #text_change 09-Jul-2004 C;Accession: S04016; JC1408; A41406; A32116; B32116; A34499; A26619; A39985; A60061; B60 R;Mosselman, S.; Hosppener, J.W.M.; Lips, C:J.M.; Jansz, H.S.
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"Hoeppener, J.W.M.; Oosterwijk, C.; Visser-Vernooy, H.J.; Lips, C.J.M.; Jansz, H.S.
"Alochhem Blophys. Res. Commun. 189, 1569-1577, 1992.
"Title: Characterization of the human islet amylaid polypeptide/amylin gene transcripts reference number: JC1408; MUID:93129228; PMID:1282806
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A;Title: Human islet amyloid polypeptide gene: complete nucleotide sequence, chromosomal A;Reference number: A41406; MUID:90114181; PMID:2608057
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R;Nishi, M.; Bell, G.I.; Steiner, D.F.
Nucleic Acids Res. 19, 6726, 1990
A;Title: Sequence of a cDNA encoding Syrian hamster islet amyloid polypeptide precursor.
A;Reference number: S13116; MUID:91067499; PMID:2251153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P23442; UNIPARC:UPI000012D0C6; EMBL:X56067; NID:g49633; PIDN
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A;Accession: B32116
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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37
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ilarity 65.7%; Pred. No. 4.8e-14;
Conservative 0; Mismatches 12.
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    golden hamster
    (golden hamster)
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NID: 932584; PIDN: CAB57803.1;

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A; Molecule type: protein
A; Residues: 50-70 < NA2>
A; Cross = references: UNIPARC:UPI0000173498
A; Experimental source: normal pancreas
A; Experimental source: normal pancreas
B; Exp. Cell Res. 183, 1899
A; Title: Islet amyloid polypeptide (IAPP): cDNA cloning and identification of an amyloid A; Reference number: A60599; MUID:89356900; PMID:2670595
A; Accession: A60599
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-89 < BBT>
A; Cross = references: UNIPARC:UPI000012D0C4
R; Christmanson, L: Rorsman, F.; Stenman, G.; Westermark, P.; Betsholtz, C.
FEBS Lett. 257, 160-166, 1990
A; Title: The human islet amyloid polypeptide (IAPP) gene. Organization, chromosomal loca
A; Recession: S10729
A; Recession: S10729
A; Recession: S10729
A; Residues: 1-89 < CHR>
A; Residues: 1-80 < CHR
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R; van Mansfeld, A.D.M.; Mosselman, S.; Hoeppener, J.W.M.; Zandberg, J.; van Teeffelen, H
Biochim. Bioc
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R;Westermark, P.; Wernstedt, C.; Wilander, E.; Hayden, D.W.; O'Brien, T.D.; Johnson, K.H Proc. Natl. Acad. Sci. U.S.A. 84, 3881-3885, 1987
A;Title: Amyloid fibrils in human insulinoma and islets of Langerhans of the diabetic ca A;Reference number: A26619; MUID:87231921; PMID:3035556
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A, Molecule type: protein
A, Molecule type: brotein
A, Residues: 34-68, / X / 7 o wES>
A, Cross-references: UNIPARC: UPI000002C9BF
B, Ccoper, G.J.S.; Willis, A.C.; Clark, A.; Turner, R.C.; Sim, R.B.; Reid, K.B.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 8628-8632, 1987
A, Title: Purification and characterization of a peptide from amyloid-rich pancreases of A, Reference number: A39985; MUID: 88068642; PMID: 3317417
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A;Residues: 34-70 <COO>
A;Cross-references: UNIPARC:UPI000002B886
A;Cross-references: UNIPARC:UPI000002B886
RS Nakazato, M.; Asai, J.; Miyazato, M.; Matsukura, S.; Kangawa, K.; Matsuo, H.
Regul. Pept. 31, 13-186, 1990
A;Title: Isolation and identification of islet amyloid polypeptide in normal human pance
A;Reference number: A60061; MUID:91219694; PMID:2091067
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A;Note: the authors obtained five independent clones for this mRNA variant, which may re R;Roberts, A.N.; Leighton, B.; Todd, J.A.; Cockburn, D.; Schofield, P.N.; Sutton, R.; Ho Proc. Natl. Acad. Sci. U.S.A. 86, 9665, 1989
A;Title: Molecular and functional characterization of amylin, a peptide associated with A;Reference number: A34499; MUID:90099324; PMID:2690069
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A,Residues: 34-70 < NAK>
A,Residues: 24-70 < NAK>
A,A.COSS-REferences: UNIPARC:UP100002B886
A,Experimental source: normal pancreas
A,Accession: B60061
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A; Residues: 30-89 < ROB>
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A;Molecule type: DNA
A;Residues: 28-89 <MO2>
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A;Molecule type: protein
A;Residues: 34, 'X', 36-39, 'S', 41-52 <WE2>
A;Residues: 34, 'X', 36-39, 'S', 41-52 <WE2>
A;Cross-references: UNIPARC:UP10000173499
R;Cort, J; Liu, Z.; Lee, G.; Harris, S.M.; Prickett, K.S.; Gaeta, L.S.L.; Andersen, N.H Biochem. Biophys. Res. Commun. 204, 1088-1095, 1994
A;Title: beta-Structure in human amylin and two designer beta-peptides: CD and NMR spect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: PC2383; MVID:95071438; PMID:7980582
A;Contents: annotation; circular dichroism and NMR studies
C;Comment: This protein is a major component of the islet amyloid deposited in the pancr
ction as a hormone.
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A;Title: Canine IAPP CDNA sequence provides important clues regarding diabetogenesis and A;Reference number: A35476; MUID:90290487; PMID:2192709
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A;Residues: 43-66, 'T' '68 <JOR>
A;Cross-references: UNIPARC:UPI000016C3DA; GB:M37720; NID:g163960; PIDN:AAA30849.1; PID:
C;Superfamily: calcitonin
                                                                                                           peptide family as an amyloid fib
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Cisuperfamily: calcitonin
Ciscupords: amidated carboxyl end; amyloid; pancreatic islet; type 2 diabetes
Ciscupords: amidated carboxyl end; predicted <SIG>
F;1-22/Domain: signal sequence #status predicted <PROI>
F;3-33/Domain: amino-terminal propeptide #status experimental <MAT>
F;3-0-70/Product: islet amyloid polypeptide #status experimental <MAT>
F;50-70/Product: islet amyloid polypeptide (17-37) #status experimental
F;53-62/Domain: carboxyl-terminal propeptide #status predicted <PRO2>
F;72-89/Domain: carboxyl-terminal propeptide #status predicted <PRO2>
F;35-40/Disulfide bonds: #status predicted
F;70/Modified site: amidated carboxyl end (Tyr) (amide in mature form from fol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: amylin precursor; IAPP; insulinoma amyloid protein
C;Species: Canis lupus familiaris (dog)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
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islet amyloid polypeptide precursor - dog
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R;Albrandt, K.; Mull, E.; Cooper, G.J.S.; Johnson, M.J.
Biochim. Biophys. Acta 1130, 97-99, 1992
A;Title: Nucleotide sequence of a cDNA for canine amylin.
A;Reference number: S22344; MUID:92182022; PMID:1543754
A;Accession: S22344
A;Cross-references: UNIPARC:UP1000016A552; EMBL:X13859; R;Westermark, P.; Wernstedt, C.; Wilander, E.; Sletten, Biochem. Biophys. Res. Commun. 140, 827-831, 1986 A;Title: A novel peptide in the calcitonin gene related A;Reference number: A26385; MUID:87048863; PMID:3535798 A;Accession: A26385
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Pred. No. 1.2e-12;
0; Mismatches 13;
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Pred. No. 4.6e-13;
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A, Map position: 12p12.3-12p12.1
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ilarity 62.9%;
Conservative 0
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Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
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NTATCATORLANFLVRTSNNLGAILSPTNVGSNTY 70

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A;Status: preliminary
A;Molecule type: mRNA; DNA
A;Residues: 1-135 c.RAN>
A;Cross-treferences: UNIPROT:Q90743; UNIPARC;UPI00000FD0B7; GB:L16955; NID:g289789; PIDN:C;Superfamily: calcitonin
C;Keywords: hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     islet amyloid polypeptide - cougar (fragment)
C;Species: Felis concolor (cougar)
C;Species: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 11-May-2000
C;Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 11-May-2000
C;Accession: A61509
R;Johnson, K.H.; Wernstedt, C.; O'Brien, T.D.; Westermark, P.
Comp. Biochem. Physiol. B 98, 115-119, 1991
A;Title: Amyloid in the pancreatic islets of the cougar (Felis concolor) is derived from A;Reference number: A61509; MUID:91284578; PMID:2060275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcitonin gene-related peptide precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00154; I50183; A24855
R;Minvielle, S.; Cressent, M.; Delehaye, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.; M
PEBS Lett. 223, 63-68, 1987
                                                                                                                                                                                                                                                                                                                                              islet amyloid polypeptide in th
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Msesidues: 1-125 <MIN-
M; Residues: 1-125 <MIN-
M; Residues: 1-125 <MIN-
M; Residues: 1-125 <MIN-
M; Route: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the
A; Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; the
M; Note: the authors translated the codon GAC for residue 56 as Glu
R; Lessonles, F; Jullienne, A; Day, F; Minvielle, S; Milhaud, G; Moukhtar, M.S.
EMBO J. 4, 2603-2607, 1985
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                                                                                                                                                              C;Species: Gallus gallus (chicken)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: As6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 2; Lt.,
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                                                                                                                                                                                                                                                                             R;Fan, L.; Westermark, G.; Chan, S.J.; Steiner, D.F. Mol. Endocrinol. 8, 713-721, 1994
A;Title: Andered gene structure and tissue axpression of A;Reference number: A56855; MUID:95021303; PMID:7935487
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Pred. No. 7.8e-10;
1; Mismatches 15;
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Mosidues: 1-29 × JOH
A;Cross-references: UNIPARC:UP1000017660F
C;Superfamily: calcitonin
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Best Local Similarity 68.v.
Best 17; Conservative
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nes 19; Conserv
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lalet amyloid polypeptide precursor - guinea pig
cispecies: Cavia porcellus (guinea pig)
Cispecies: Cavia porcellus (guinea pig)
Cispecies: 21-Feb-1990 #sequence_revision 04-Sep-1992 #text_change 09-Jul-2004
Ciscession: D33542
R;Nishi, M.; Chan, S.J.; Nagamatsu, S.; Bell, G.I.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 5738-5742, 1989
A;Title: Conservation of the sequence of islet amyloid polypeptide in five mammals is cc
A;Reference number: A33542; MUID:89345542; PMID:2668946
A;Accession: D33542
A;Accession: D33542
A;Molecule type: mRNA
A;Residues: 1-92 - NIS>
A;Coss-references: UNIPROT:P12966; UNIPARC:UPI000012D0C2; GB:WZ5387; NID:g191271; PIDN:
A;Coss-references: UNIPROT:P12966; UNIPARC:UPI000012D0C2; GB:WZ5387; NID:g191271; PIDN:
C;Superfamily: calcitonin
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A,Residues: 34, X',36-39, X',41-60 <WES>
A,Cross-references: UNIPARC:UPI00002C9C0
C,Superfamily: calcitonin
C,Keywords: amidated carboxyl end; amyloid; pancreas
F;70/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
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A,Residues: 189 cNIS>
A,Cross-references: UNIPROT:P12967; UNIPARC:UPI000012D0C3; GB:M25388; NID:g163861; PIDN:
R,Cross-references: UNIPROT:P12967; UNIPARC:UPI000012D0C3; GB:M25388; NID:g163861; PIDN:
R) Establiz, C.; Christmanson, L.; Engstroem, U.; Rorsman, F.; Jordan, K.; O'Brien, T.D.
Diabetes 39, 118-122, 1990
A,Title: Structure of cat islet amyloid polypeptide and identification of amino acid res
A,Reference number: A60499
A,Reference number: MO499
A,Status: not compared with conceptual translation
A,Molecule type: mRNA
A,Residues: 34-70 cBET>
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R;Westermark, P.; Wernstedt, C.; Wilander, E.; Hayden, D.W.; O'Brien, T.D.; Johnson, K.H
Proc. Natl. Acad. Sci. U.S.A. 84, 3881-3885, 1987
A;Title: Amyloid fibrils in human insulinoma and islets of Langerhans of the diabetic ca
A;Reference number: A26619; WUID:87231921; PMID:303556
A;Accession: B26619
A;Status: preliminary
                                                                                                               islet amyloid polypeptide precursor - cat
C;Species: Relia silvestris catus (domestic cat)
C;Decies: Relia silvestris catus (domestic cat)
C;Dacession: A35542; A60499; B26619
R;Nishi, M.; Chan, S.J.; Nagamatsu, S.; Bell, G.I.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 5738-5742, 1989
A;Title: Conservation of the sequence of islet amyloid polypeptide in five mammals is A;Reference number: A35542; MUID:89345542; PMID:2668946
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Pred. No. 1.9e-12;
0; Mismatches 13; Indels
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62.9%;
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Best Local Similarity 62.9
Matches 22; Conservative
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Query Match
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Matches 9; Conserv
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A; Residues: 1-72 <RES>
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C;Species: Orycclagus cuniculus (domestic rabbit)
C;Species: Orycclagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I.46934
R;Christmanson, L.; Betsholtz, C.; Leckstrom, A.; Engstrom, U.; Cortie, C.; Johnson, K.H
Diabetologia 36, 183-188, 1993
A;Title: Islet amyloid polypeptide in the rabbit and European hare: studies on its relath
A;Reference number: 146933; MUID:93215963; PMID:8462765
A;Accession: 146934
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-23 CGHR>
A;Cross-references: UNIPROT:Q07334; UNIPARC:UPI000016C61B; GB:S57804; NID:g299058; PIDN:C;Superfamily: calcitonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       islet amyloid polypeptide - European hare (fragment)
C;Species: Lepus capensis europaeus (European hare)
C;Species: Lepus capensis europaeus (European hare)
C;Date: 2.1-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146933
R;Christmanson, L.; Betsholtz, C.; Leckstrom, A.; Engstrom, U.; Cortie, C.; Johnson, K.H Diabetologia 36, 183-188, 1993
A;Title: Islet amyloid polypeptide in the rabbit and European hare: studies on its relath A;Reference number: 146933; MUID:93215963; PMID:8462765
A;Accession: 146933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Title: Elucidation of the nucleotide sequence of chicken calcitonin mRNA: direct evide A,Reference number: A25725, MUID:86030240; PMID:4054101
A;Contents: annotation
R;Minvielle, S.; Cressent, M.; Lasmoles, F.; Jullienne, A.; Milhaud, G.; Moukhtar, M.S. FEBS Lett. 203, 7-10, 1986
A;Title: Isolation and partial characterization of the calcitonin gene in a lower verteb A;Reference number: I50183; MUID:86248126; PMID:3487468
                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA.
A;Residues: 74-125 <MIZ.>
A;Residues: 74-125 <MIZ.>
A;Cross-references: UNIPARC:UPIO0001712BC; GB:D00007; NID:g222801; PIDN:BAR00006.1; PID.
C;Comment: The calcitonin gene codes for two mRNA species by tissue-specific alternative ripheral nervous system codes for calcitonin gene-related peptide.
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*Residues: 1-23 cCHR>
A;Cross-references: UNIPROT:Q07333; UNIPARC:UPI000012D0C5; GB:S57802; NID:g299056; PIDN:
C;Superfamily: calcitonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Introns: 29/2; 73/2
C;Superfamily: calcitonin
C;Keywords: alternative splicing; amidated carboxyl end; neuropeptide
C;Keywords: alternative splicing; amidated peptide #status predicted <MAT>
F;80-116/Product: calcitonin gene-related peptide #status predicted
F;81-86/Disulfide bonds: #status predicted
F;81-86/Modified site: amidated carboxyl end (Phe) (amide in mature form from following
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 NTATCVTHRLADFLSRSGGVGKNNFVPTNVGSKAF 116
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                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 9; Conserv
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calcitonin gene-related peptide beta precursor - human N;Alernate names: calcitonin gene-related peptide II C;Species: Home sapiens (man) C;Species: Home sapiens (man) C;Species: Home sapiens (man) C;Species: Jo-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004 C;Accession: A25864; JH0620; B26142; A34565 R;Steenbergh, P.H.; Hoeppener, J.W.M.; Zandberg, J.; Visser, A.; Lips, C.J.M.; Jansz, H. FEBS Lett. 209, 97-103, 1986 A;Fitles: Structure and expression of the human calcitonin/CGRP genes. A;Reference number: A25864; MUID:87105923; PMID:3492393
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A; Residues: 82, X', 84-87, X', 89-91, X', 93-98, X', 100-105, X', 107-109 < PET>
A; Residues: 82, X', 84-87, X', 84-87, X', 84-87, X', 107-109 < PET>
A; Cross references: UNIPARC: UP10000176611
R; Minalawansa, S.J; Morris, H.R.; Etienne, A.; Blench, I.; Panico, M.; MacIntyre, I.
Biochem. Biophys. Res. Commun. 167, 993-1000, 1990
A; Title: Isolation, purification and characterization of beta-hCGRP from human spinal co-A; Reference number: A34565; MUID: 90211348; PMID: 2332288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P10092; UNIPARC:UP1000016A6C1; EMBL:X02404; NID:g29933; PIDN C;Superfamily: calcitonin
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R; Petermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.
J. Biol. Chem. 262, 542-545, 1987
A; Title: Identification in the human central nervous system, pituitary, and thyroid of A; Reference number: A92637; MUID:87109142; PMID:3492492
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: 137232
R;Steenbergh, P.H.; Hoppener, J.W.; Zandberg, J.; Lips, C.J.; Jansz, H.S.
FEBS Lett. 183, 403-407, 1985
A;Title: A second human calcitonin/CGRP gene.
A;Reference number: 137232; MUID:85180007; PMID:2985435
A;Accession: 137232
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                            Gaps
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A;Title: Isolation and characterization of peptides which act on rat pla A;Reference number: JH0618; MUID:92287083; PMID:1318039
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Length 23
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A;Residues: 1-127 <STE>
A;Cross-references: UNIPROT:P10092; UNIPARC:UPI0000126E36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.9%; Score 43; DB 2; Le
Best Local Similarity 34.3%; Pred. No. 0.27;
Matches 12; Conservative 1; Mismatches 22;
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    Score 43; DB 2;
Pred. No. 0.076;
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                                                                                0; Mismatches
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A;Residues: 82,'X',84-87,'X',89-104 <KIT>
A;Cross-references: UNIPARC:UP10000176610
    30.9%;
                                                                                                                                                                                                                      1 TORLANFLIHSSNNFG 16
                                                                                                                                                             TORLXNFLXXXXXNXG
                                                                            Conservative
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calcitonin gene-related peptide - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0709
R;Miyata, A.; Jiang, L.; Minamino, N.; Arimura, A.
R;Miyata, A.; Jiang, L.; Minamino, N.; Arimura, A.
A;Title: Identification of calcitonin gene related peptide in ovine hypothalamic extract A;Reference number: JH0709; MUID:93038624; PMID:1417824
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A; Residues: 1-128 ANNA-
A; Residues: 1-128 ANNA-
A; Cross-references: UNIPROT: P01256; UNIPARC: UPI00001708AA; GB:L29188; GB:J00714; GB:N000
R; Jonas, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermod, J.J.; Bvans, R.
R; Jonas, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermod, J.J.; Bvans, R.
Proc. Natl. Acad. Sci. U. S.A. 82, 1994-1998, 1985
A; Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related p
A; Reference number: A94030; MUID:85166259; PMID:3872459
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C;Keywords: alternative splicing; predicted <SIG>
F;1-25/Domain: signal sequence #status predicted <SIG>
S;3-119/Product: aaltitoring sene-related peptide #status predicted <MAT>
F;84-89/Disulfide bonds: #status predicted
F;119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl
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A;Reference number: A01524; MUID:82220111; PMID:6283379
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Cispecies: Ratus norvegiums (Norway rat)
Cibace: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
Cibacession: A01524; B22949
R;Amara, S.G.; Jonas, V.; Rosenfeld, M.G.; Ong, E.S.; Evans, R.M.
Nature 298, 240-244, 1982
A;Title: Alternative RNA processing in calcitonin gene expression generates
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Gaps
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A,Experimental source: hypothalamus
C,Comment: This protein has adenylate cyclase stimulating activity.
C;Superfamily: calcitonin
C;Superfamily: amidated carboxyl end, neuropeptide
F;37/Modified site: amidated carboxyl end (Phe) #status experimental
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.2%; Score 42; DB 1; 34.3%; Pred. No. 0.83;
                                                                                                                                                                     TIPKOFITNYL-AACRNGGGTLPDAGVTSNTW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-39,'A',40-49,'L',50-67,70-128 <JON>
A;Cross-references: UNIPARC:UP10000126E33
C;Superfamily: calcitonin
                                                                                     TXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
Mismatches
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Matches 12, Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-37 <MIY>
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Best Local Similarity
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12;
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Matches
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A;Cross-references: UNIPARC:UP10000179C77; EMBL:U21319; NID:g687832; PID:g687833; PIDN:A
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer membrane protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64521
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;118/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 388, 539-547, 1997

A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A; Reference number: A64520; MUID:97394467; PMID:9252185

A; Reference number: A64520; MUID:97394467; PMID:9252185

A; Reference number: A64520; MUID:9739467; PMID:9252185

A; Reference type: DNA

A; Molecule type: DNA

A; Residues: 1-634 < TOM>
A; Residues: 1-634 < TOM>
A; Cross-references: UNIPROT:092N51; UNIPARC:UPI0000165585; GB:AE000511; TIGR:HP0009
                                     A;Residues: 82-86;104-117 <WIM>
A;Cross-references: UNIPARC:UP10000176612; UNIPARC:UP10000176613
C;Comment: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.
C;Genetics:
A;Genetics:
A;Genetic
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacte: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15718
R;Latreille, P.
Submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid C30G12.
A;Reference number: Z18393
A;Recession: T15718
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Bolcule type: DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.9%; Score 43; DB 2; Length 127;
llarity 34.3%; Pred. No. 0.52;
Conservative 1; Mismatches 22; Indels
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A;Gene: CESP:C30G12.1
A;Introns: 37/3; 71/2; 107/3; 153/2; 205/1; 289/1; 376/3
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nes 12, Conserv
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Matches
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A;Cross-references: UNIPROT:P10093; UNIPARC:UPI0000126E39; GB:M1596; NID:9203232; PIDN: A;Note: the authors translated the codon AAA for residue 47 as Phe, and CGC for residue R;Wang, M.W.; Young, A.A.; Rink, T.J.; Coopet, G.J.S. FEBS Lett. 291, 195-198, 1991
FFBS Lett. 291, 195-198, 1991
A;Title: (8-37)h-CGRP antagonizes actions of amylin on carbohydrate metabolism in vitro A;Reference number: S18300; MUID:92038032; PMID:1936264
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submitted to the EMBL Data Library, July 1999
A;bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: E75101
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A;Residues: 1-89 «KAM»
A;Cross-references: UNIPROT:Q9UZES; UNIPARC:UPI0000633E1; GB:AJ248286; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Wambutr, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 134;
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-990 «MMA>
A;Cross-references: UNIPROT:Q9UG03; UNIPARC:UPI0000071BED;
A;Experimental source: fetal brain; clone DKFZp564F0923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.5%; Score 41; DB 2;
Best Local Similarity 34.3%; Pred. No. 1.4;
Matches 12; Conservative 1; Mismatches 2;
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Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 96-104,'S',106-112,'N',114-125 <WAN>
A;Cross-references: UNIPARC:UP1000003515C
C;Superfamily: calcitonin
C;Keywords: neuropeptide
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61.5%;
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Best Local Similarity 61...
Best Local 8; Conservative
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B44173
calcitonin gene-related peptide alpha precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Species: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C;Accession: 844173
R;Amara, SG.; Arriza, J.L.; Leff, S.E.; Swanson, L.W.; Evans, R.M.; Rosenfeld, M.G.
Science 229, 1094-1097, 1985
A;Title: Expression in brain of a messenger RNA encoding a novel neuropeptide homologous
A;Accession: B44173
A;Accession: B44173
A;Accession: B44173
A;Accession: B44173
A;Accession: B44173
A;Residues: 1-128 <AMA>
A;Stetuences: UNIPROT:P01256; UNIPARC:UPI0001708AB; GB:M11597; NID:g203226; PIDN:
A;Accession: the authors translated the codon CGC for residue 99 as Ser
C;Superfamily: calcitonin
C;Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A44173
A4
                                                                                                                    probable outer membrane protein - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
G;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004
C;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004
C;Accession: A71986
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MuID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-668 <ARN>
A;Cross-references: UNIPROT:Q9ZN51; UNIPARC:UPI0000D35B7; GB:AE001440; GB:AE001439; NIL
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0007
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Best Local Similarity 34.3
Matches 12; Conservative
                                                                      RESULT 21
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C;Accession: ĴQ1534
R;Taguchi, F.; Ikeda, T.; Shida, H.
J. Gen. Virol. 73, 1065-1072, 1992
A;Title: Molecular cloning and expression of a spike protein of neurovirulent murine cor
A;Reference number: JQ1534; MUID:92268864; PMID:1316938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Parker, S.E.; Gallagher, T.M.; Buchmeier, M.J. Virology 173, 664-673, 1989
Virology 173, 664-673, 1989
A; Title: Sequence analysis reveals extensive polymorphism and evidence of deletions with A; Reference number: A33748; MUID:90085815; PMID:2556846
                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:Q8ZAV3; UNIPARC:UPI00000CDA68; GB:AL590842; PIDN:CAC93150.1,
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A;Residues: 1-1376 «PAR»
A;Cross-references: UNIPROT:P22432; UNIPARC:UPI000013866B; GB:M32789; NID:g331846; PIDN
C;Superfamily: coronavirus E2 glycoprotein
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Mature 413, 523-527, 2001
AjTitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: glycoprotein; transmembrane protein
F1-14/Domain: slignal sequence #status predicted <SIG>
F1-14/Domain: slignal sequence #status predicted <EGO>
F;15-1376/Product: E2 glycoprotein #status predicted <EGB>
F;15-769/Product: 90B glycoprotein #status predicted <EGB>
F;170-1376/Product: 90B glycoprotein #status predicted <EGA>
F;1316/Product: 90B glycoprotein #status predicted <EGA>
F;1316/Product: 90B glycoprotein #status predicted <EGA>
F;31,00-136/192,357,435,677,709,717,789,806,945,1232,1242,1261,1277,1298/Binding site:
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NiAlternate names: peplomer glycoprotein; spike glycoprotein
NiContains: 90A glycoprotein; 90B glycoprotein
Cispecies: murine hepatitis virus, MHV
Cispecies: 30-Sep-1993 #sequence_revision 30-Søp-1993 #text_change 09-Jul-2004
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A;Residudes: 1.1376 <TRAC
A;Residudes: L.1376 <TRAC
A;Cross-references: UNIPROT:Q02385; UNIPARC:UPI000013866D; DDBJ:D10255
A;Note: the authors translated the codon TTT for residue 8 as Leu, GGG
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Pred. No. 28;
3; Mismatches 20; Indels
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Pred. No. 49;
0; Mismatches
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C,Superfamily: coronavirus E2 glycoprotein
C,Keywords: glycoprotein; transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 28.1%;
1 Similarity 30.3%;
10; Conservative 3
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Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                       A, Accession: AB0448
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-833 «KUR»
A, Cross-references: UNIPR
C, Genetics:
A, Gene: YPO3681
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                  D8759

D8759

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C; Daceis Caulobacter crescentus

C; Daceis Caulobacter crescentus

C; Daceis D8759

E; Datein D8759

E; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

M. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. US.A. 98, 4136-4141, 2011

A; Title: Complete Genome Sequence of Caulobacter crescentus.

A; Reference number: A87249; MUD:21173698; PMID:11259647

A; Refatus: preliminary

A; Molecule type: DNA

A; Mesidue: 1-384 <STO>

A; Cometics: C; Cigenetics: UNIPROT:09A4K3; UNIPARC:UPI00000C7869; GB:AE005673; NID:g13424436; E
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C;Species: Yersinia pestis
C;Daces 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0448
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: FOR632222-633439
C;Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Length 384;
Pred. No. 12;
3; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h Similarity 27.3%; Pred. No. 12; Jength 405; 9; Conservative 4; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 Arparddiastirqidaerpparpiriuvpqrp 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230
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30.3%;
       109 GPRLPDTFLGSAT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CC2828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
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A64388
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Matches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 179-381, T', 383-413, 'P', 415-925 (2004)
A;Cross-references: UNIPARC: UDIO000176755; EMBL:AF036703; PIDN:AAB88554.1; GSPDB:GN00022
A;Experimental source: strain Bristol N2; clone T11F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S23443
R;Chen, J.C.; Mortenson, D.B.
Biochim. Biochys. Acta 1131, 199-202, 1992
A;Title: Identification of six open reading frames from a region of the Azotobacter vine A;Reference number: S23438; MUID:92305060; PMID:1610901
A;Accession: S23443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1379 <CHE>
A;Cross-references: UNIPROT:P31882; UNIPARC:UPI000012D03F; EMBL:X63650; NID:g39239; PIDN C;Superfamily: [NiFe]-hydrogenase maturation factor, HypD type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T11064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-474 <FUL>
A;Cross-references: UNIPROT:Q9GXJ8; UNIPARC:UPI0000075DC4; EMBL:U64605; PIDN:AAB04590.2
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                  A;Map position: 4
A;Introns: 19/3; 203/3; 487/1; 550/3; 620/2
A;Introns: 19/3; 203/3; 487/1; 550/3; 620/2
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology; F;1-26/Domain: signal sequence #status predicted <SIG>F;27-925/Product: lipoprotein receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 8 - Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: X
A;Introns: 39/2; 80/2; 112/1; 179/3; 265/3; 308/3; 330/1; 433/2
A;Note: C05D9.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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A;Description: The sequence of C. elegans cosmid T11F8. A;Reference number: Z21191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: The sequence of C. elegans cosmid CO5D9. A; Reference number: Z20960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%; Score 38; DB 2; ilarity 36.4%; Pred. No. 49; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ARAGTLQLDGFI-----GPAHVSTVIGSBAY 212
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submitted to the EMBL Data Library, September 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 NILKSRFDGSNPSAPTTFVGHN 133
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Best Local Similarity 30.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                   A, Gene: lr; CESP:T11F8.3
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Matches 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                    A; Accession: T32559
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                                                                                                                                                                                                                                                                        C;Genetics:
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A; Residues: 1-1662 <COR>
A; Residues: 1-1662 <COR>
C; Cose-references: UNIPROT: P71431; UNIPARC: UPI00000BE9CF; EMBL: Z25774; NID: e1427784; PI
C; Genetics:
A; Note: mofA
F; 1-33/Domain: signal sequence #status predicted <SIG>
F; 1-362/Product: mofA protein #status predicted <MAT>
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-925 <TAN>
A; Cross-references: UNIPROT: Q9UB94; UNIPARC: UPI00000812C2; EMBL: U62639; PIDN: AAD09364.1
A; Experimental source: strain Bristol N; clone CB1007
A; Tang, P.; Kingston, 1.B.
Bubmitted to the EMBL Data Library, June 1996
A; Description: Cloning and characterization of a lipoprotein receptor gene from the nema
A; Reference number: Z21713
   C;Keywords: glycoprotein; transmembrane protein
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-1376/Product: B2 glycoprotein #status predicted <EGS>
F;15-169/Product: 90B glycoprotein #status predicted <EGB>
F;15-169/Product: 90A glycoprotein #status predicted <EGB>
F;170-1376/Product: 90A glycoprotein #status predicted <EGA>
F;1321-1338/Domain: transmembrane #status predicted <TMN>
F;31,60,134,192,357,435,442,582,677,709,717,740,789,806,896,945,1178,1232,1242,1261,1277
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C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T18540
S;Corseljens, P.L.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z18959
A;Accession: T18540
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Rosidudes: 1-129, TL', 131-269, R', 271-819, 'L', 821-925 <TA2>
A;Cross.references: UNIPARC:UD1000007DEE9; EMBL:U62281; PIDN:AAD09363.1
A;Experimental source: strain Bristol N2
B;Johnson, D.
submitted to the EMBL Data Library, December 1997
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                                                                                                                                                                                                                                      DB 1; Length 1376;
                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Leptothrix discophora
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                                                                                                                                                                                                                                                                        Score 39; DB Similarity 57.1%; Pred. No. 49; 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 GPHLRSARVGSGTY 528
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Best Local Similarity
Matches 8, Conserva
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probable transcription regulator LYSR-type [imported] - Escherichia coli (strain 0157:H7 c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: Escherichia coli (c; Species: 18-Jul-2004 (c; Species: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8X4T4; UNIPARC:UPI00000D0D7E; GB:BA000007; PIDN:BAB35333.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: C68751
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q8X4T4; UNIPARC;UPI00000D07E; GB:AE005174; NID:g12515432; P
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                            C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0309
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50.0%; Pred. No. 22;
tive 1; Mismatches
                                                                                                                     Score 37; DB 2;
Pred. No. 15;
0; Mismatches
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7
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Pred. No.
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C,Superfamily: hypothetical protein b1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: hypothetical protein b1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.6%;
50.0%;
                                                                                                                     Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                   109 NPGSQLPYTQVGPN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :| ||| |
161 GPDIPMAIVGSPDY 174
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                                                                                                                                                                                                                                                                          22 NXGPXLPXTXVGSN 35
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Best Local Similarity
Matches 7; Conserv
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hes 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-299 <HAY>
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A;Gene: ML2522
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: G87224
R;Cole, S. T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R;Cole, S. T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
R; Davies, R.M.; Devlin, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G87224
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <570>
A;Residues: 1-218 <570>
A;Coss-references: UNIPROT:Q9CD38; UNIPARC:UPI0000C6C72; GB:AL450380; NID:g13093788; E
C;Genetics:
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                                                Gaps
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Pred. No. 8.4e+02;
2; Mismatches 19; Indels 1;
                                                Indels
                                            12;
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    35.7%; Pred. No. 29; tive 3; Mismatches
                                                                                                                                                                         363 TQNVQNFLNSFITNVG---NFTSTGNDT 387
                                                                                                                     27.0%;
        Best Local Similarity 35.7
Matches 10; Conservative
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Matches 12; Conserv
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A;Residues: 1-389 <WIL>
A;Cross-references: UNIPROT:Q21081; UNIPARC:UPI0000080155; EMBL:Z49068; PIDN:CAA88855.1; A;Experimental source: clone K01C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Reduces: 1,420 < POS>
A) Cross-references: UNIPROT: P53616; UNIPARC: UPI000013621B; EMBL: X86470; NID: 9791101; PID
A) Cross-references: UNIPROT: P53616; UNIPARC: UPI000013621B; EMBL: X86470; NID: 9791101; PID
A) Cross-references: Doignon, F.; Crouzet, M.
A) Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV
A) Reference number: S58711; MUID: 96021608; PMID: 8533472
A) Accession: S58712
A) Accession: S58712
A) Status: nucleic acid sequence not shown; translation not shown
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A;Residues: 1-420 cms.
A;Cross-references: UNIPARC:UPI000013621B; EMBL:U12141; NID:g1314216; PIDN:AAA99645.1; P.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast 12, 391-402, 1996
A;Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12
A;Reference number: S63925; MUID:96267764; PMID:8701611
A;Accession: S63945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
           hypothetical protein KOIC8.2 - Caenorhabditib elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tasle: 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23167
R;Sins, M.
Submitted to the EMBL Data Library, April 1995
A;Reference number: Z19702
A;Accession: T31367
A;Accession: T31367
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: protein NZ41; protein YN4066w; protein YNL1612
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53916; S58712; S62994; S62998; S63945
R;Pochlmann, R.; Philippsen, P.
R;Pochlmann, R.; Philippsen, P.
A;Reference number: S53896
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submitted to the Protein Sequence Database, April 1996
A;Reference number: S62997
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30;
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Pred. No.
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A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0%
Them 9; Conservative
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A; Residues: 1-420 <BEF>
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probable transcription regulator ycjZ - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C64882
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Actuse: prellminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-299 kBLAT>
A;Cross-references: UNIPROT:P77333; UNIPARC:UP1000013A6EA; GB:AE000231; GB:U00096; NID:g
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Genetics:
C;Superfamily: hypothetical protein b1328
C;Keywords: DNA binding; transcription regulation
F;20-50/Region: regulatory protein lysR motif
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HAVZAX

HANGAX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 2
Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GPDIPMAIVGSPDY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.6
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.6
Best Local Similarity 46.7
Matches 7; Conservative
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252 NDNDTVPSTTVGSST 266

RESULT 41

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A.Cross-references: UNIPROT:P23253, UNIPARC!UPI0000136AE0; GB:M61732; NID:g162302; PID:g
A;Note: the authors translated the codon TCT for residue 45 as Cys
C;Comment: This protein plays a role in parasite-host cell interaction.
C;Comment: Trypomastigote-specific surface antigen
C;Keywords: glycoprotein; glycosidase; hydrolase
F;394/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaccesion: H96650

RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Y.; Liu, X.; Liu, X.; Liu, Z.X.; Liu, Z.X.; Liu, Z.X.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome i of the plant Arabidopsis.

A;Accession: H96650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: genomic RNA
A;Residues: 1-175 <GUI>
A;Cross-references: UNIPARC:UPI00000F5803; EMBL:X83110; NID:g951030; PIDN:CAA58174.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q95XF0; UNIPARC:UP100000A7A83; GB:AE005173; NID:g5454189; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein T3P18.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear dress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable movement protein - beet mild yellowing virus
C;Species: beet mild yellowing virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 2; Length 130 Pred. No. 1.2e+02; O; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S65828
R;Guilley, H.; Richards, K.E.; Jonard, G.
Arch. Virol. 140, 1109-1118, 1995
A;Title: Nucleotide sequence of beet mild yallowing virus RNA.
A;Reference number: S65825; MUID:95336315; PMID:7611881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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C;Superfamily: potato leaf roll virus genome-linked protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%; Score 37; DB 2;
27.3%; Pred. No. 1e+02;
tive 4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.3%; Score 36.5; Dilarity 35.3%; Pred. No. 15; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: retrovirus-related polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.6%;
ilarity 61.5%;
Conservative
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.33
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-1309 <STO>
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Best Local Similarity
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nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S:
Matches 12
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ENDING 193

ENDING 193

ENDING 193

ENDING 193

ENDING 193

Hypothetical protein F5Al3.3 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E96492

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nature 408, 816-820, 200

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cosa-references: UNIPARC:UPI000013621B; EMBL:X86470; NID:g791101; PIDN:CAA60196.1; PI
C;Genetics: A;Molecule sequence was submitted to the EMBL Data Library, April 1995
A;Gene: SGD:SUN4
A;Crosa-references: SGD:S0005010; MIPS:YNL066w
A;Map position: 14L
A;Genome: nuclear
C;Superfamily: Saccharomyces NCA3 protein
C;Superfamily: Saccharomyces NCA3 protein
F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;46-420/Product: SUN4 protein #status predicted <MAT>
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Wildersalidase (EC 3.2.1.18) - Trypanosoma cruzi
WiAlternate names: neuraminidase
CiSpecies Trypanosoma cruzi
CiDate: 30-Uun-1992 #sequence_revision 30-Uun-1992 #text_change 09-Uul-2004
CiAccession: JH0557
CiAccession: JH0557
Wed. 174, 179-191, 1991
A;Title: The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial neu A;Reference number: JH0557; MUID:91277609; PMID:1711561
A;Reference number: JH0557
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT: Q9FZH1; UNIPARC: UPI00000A0ED7; GB:AE005173; NID:g9802762; C;Genetics:
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C;Superfamily: Arabidopsis thaliana hypothetical protein T24H24.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.6%; Score 37; DB Best Local Similarity 33.3%; Pred. No. 32; Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.6%; Score 37; DB ilarity 28.1%; Pred. No. 43; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 NMVIPTYVQAGDSLPLTVVDQDTY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 NFLXXXXXXXXGPXLPXTXVGSNTY 37
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Best Local Similarity
Matches 9; Conserv:
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A;Molecule type: DNA
A;Residues: 1-538 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: F5A13.3
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A;Molecule type: DNA
A;Residues: 1-3092 <BEC>
A;Cross-references: UNIPROT:P18963; UNIPARC:UPI000012D874; EMBL:236009; NID:9536437; PID
                                                                                                                      A; Experimental source: strain S288C
R; Becam, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos, Vests 10 (Suppl.A), S1-S11, 1994
A; Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete A; Reference number: S46569; MUID:94378717; PMID:8091856
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 2768-3092 <BEZ>
A; Cross-references: UNIPARC: UP10000168A27; EMBL:X75891; NID:g496856; PIDN:CAA53498.1; PI
A; Experimental source: strain S288C
R; Zagulski, M.; Becam, A.M.; Grzybowska, E.; Lacroute, F.; Migdalski, A.; Slonimski, P.P
Fast 10, 1277-1234, 1994
A; Title: The sequence of 12.5 kb from the right arm of chromosome II predicts a new N-te
A; Reference number: S46619; MUID:95274325; PMID:7784712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Tanaka, K.; Matsumoto, K.; Toh-e, A. Mol. cell. Biol. 9, 757-768, 1989
A; Title: IRA1, an inhibitory regulator of the RAS-cyclic AMP pathway in Saccharomyces ce A; Reference number: A30135; MUID:89219070; PMID:2540426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 155-360,'G',362-3092 <TAN>
A;Cross-references: UNIPARC:UPI0000168C89; EMBL:M24378; NID:g295615; PIDN:AAA34709.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 2R
C;Superfamily: regulatory protein IRA2; ras-specific GAP catalytic domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3092;
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F;1187-1204/Domain: transmembrane #status predicted <TW8>
F;1187-1442/Domain: transmembrane #status predicted <TW8>
F;1449-1465/Domain: transmembrane #status predicted <TW19>
F;1696-1712/Domain: transmembrane #status predicted <TW10>
F;1696-1712/Domain: transmembrane #status predicted <TW10>
F;1850-1868/Domain: transmembrane #status predicted <TW13>
F;2366-2344/Domain: transmembrane #status predicted <TW13>
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transmembrane #status predicted <TM15>
transmembrane #status predicted <TM16>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;238-254/Domain: transmembrane #status predicted <TM2>F;291-307/Domain: transmembrane #status predicted <TM3>F;791-387/Domain: transmembrane #status predicted <TM4>F;671-687/Domain: transmembrane #status predicted <TM4>F;664-680/Domain: transmembrane #status predicted <TM5>F;801-817/Domain: transmembrane #status predicted <TM5>F;801-817/Domain: transmembrane #status predicted <TM5>F;801-817/Domain: transmembrane #status predicted <TM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: phosphoprotein; transmembrane protein
F;93-109/Domain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Pred. No. 3.8e+02,
2; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: SGD:S0000344; MIPS:YBR140c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status
transmembrane #status
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A;Cross-references: UNIPARC:UPI00001764E1
A;Experimental source: strain S288C
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36.7%;
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Best Local Similarity
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F;2751-2767/Domain:
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Accession: S46009
                                                                                                                                                                                                                                                                                                            A;Accession: S46582
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C187374
S-layer protein RsaA [imported] - Caulobacter crescentus
C187374
S-layer protein RsaA [imported] - Caulobacter crescentus
C18pecies: Caulobacter crescentus
C2 Selabary, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
C2 Selabary, R.T.; Dodson, R.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: C87374
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Modecule type: nucleic acid
A;Residues: 1-1026 <GIL>
A;Cross-references: UNIPROT: P35828; UNIPARC: UPI000005415D; GB:AF062345; GB:M22663; GB:M8
A;Experimental source: CB15A, ATCC 19089
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:116173, NCBIP:116174)
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A;Cross-references: UNIPARC:UP10000165C01; GB:AE005673; NID:g13422297; PIDN:AAK22991.1;
C;Genetics:
                                                                                                                                                                                                                                     paracrystalline surface layer protein RsaA - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48995
R;Gilchrist, A.; Fisher, J.A.; Smit, J.
Can. J. Microbiol. 38, 193-202, 1992
A;Title: Nucleoride sequence analysis of the gene encoding the Caulobacter crescentus payetence number: A48995; MUID:93007489; PMID:1393820
A;Status: preliminary
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GTPase-activating protein IRA1 - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein YBR1016; protein YBR140c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S46009; S45582; S46619; A30135
R;Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.
A;Reference number: S45995
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                                                                                  140 NPAGGHLQRLTS-----TGRTGMTLPRTNSGSST 168
                                   3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNT 36
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es 12; Conserva
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hes 12; Conserv
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Biochem. Biophys. Res. Commun. 123, 648-655, 1984
A;Title: Structure and expression of a gene encoding human calcitonin and calcitonin gen
A;Reference number: I52204; MUID:85022523; PMID:6148938
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000016A6CO; dB:K03512; NID:g180465; PIDN:AAA52011.1; PID: R;Craig, R.K.; Riley, J.H.; Edbrooke, M.R.; Broad, P.M.; Foord, S.M.; Al-Kazwini, S.J.; Bichem. Soc. Symp. 52, 91-105, 1986
A;Title: Expression and function of the human calcitonin/alpha-CGRP gene in health and d A;Reference number: 139387; MUID:87213363; PMID:3034287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 77-128 <RES.>
A; Residues: 77-128 <RES.>
A; Cromes references: WIPPARC: UPI000016A651; GB:MZ6094; NID:g179798; PIDN:AAA51912.1; PID:
C; Comment: This peptide is a potent vasorelaxant.
C; Comment: This peptide increases the rate and force of contraction of rat auricles in v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: alternative splicing; amidated darboxyl end; neuropeptide; vasodilator 883-119/Product: calcitorin gene-related peptide alpha #status experimental <CTN>F:64-89/Disulfide bonds: #status experimental F:191-Modified site: amidated carboxyl end {Phe} (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 DTATCVTHRLAGLLSRSGGVVKNNFVPTNVGSKAF 119
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Job time : 42 secs
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A;Map position: 11p15.2-11p15.1
A;Introns: 29/2; 76/2
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                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 48-119 <RE2>
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                      A; Accession: I52204
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N;Alternate names: calcitonin gene-related peptide I; CGRP-I
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1987 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Accession: 807644; A22949; B22716; I55536; JJ0005; S10813; A26142; JH0619; I52204; I84
R;Broad, P.M.; Symes, A.J.; Thakker, R.V.; Craig, R.K.
Nucleic Acids Res. 17, 6999-7011, 1989
A;Title: Structure and methylation of the human calcitonin/alpha-CGRP gene.
A;Reference number: 807643; MUD: 89386053; PMID: 2571128
A;Accession: 807644
A;Accession: 807644
A;Residues: 1-128 <BRO
A;Residues: 1-128 <BRO
A;Cross-references: UNIPROT: P06881; UNIPARC: UP10000126E30; EMBL:XI5943; NID: G29613; PIDN
A;Note: the authors translated the codon CAG for residue 19 as Glu
A;Note: the authors translated the codon CAG for residue 19 as Glu
A;Note: the authors (Sci. U.S.A. 82, 1994-1998, 1988
A;Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related p
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Cross-references: UNIPARC:UPI000016A651; GB:M28637; NID:9180467; PIDN:AAA52012.1; PID:
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A;Title: Isolation and characterization of peptides which act on rat platelets, from a
A;Reference number: JH0618; MUID:92287083; PMID:1318039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Cross-references: UNIPARC:UP1000017349B
;Petermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.
- Biol. Chem. 262, 542-545, 1987
:Title: Identification in the human central nervous system, pituitary, and thyroid of ;Reference number: A92637; MUID:87109142; PMID:3492492
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R, Nelkin, B.D.; Rosenfeld, K.I.; de Bustros, A.; Leong, S.S.; Roos, B.A.; Baylin, S.B.
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A,Molecule type: mRNA
A,Residues: 1-128 - 40N.
A,Residues: 1-128 - 40N.
A,Cross-references: UNIPARC: UDI0000126E30; GB:M12667; NID:g179825; PIDN:AAA51914.1; PR; Edbrooke, M.R.; Parker, D.; McVey, J.H.; Riley, J.H.; Sorenson, G.D.; Pettengill, CBMBO J. 4, 715-724, 1985
A;Title: Expression of the human calcitonin/CGRP gene in lung and thyroid carcinoma. A;Reference number: A91034; MUD:85230541; PMID:2408883
A;Accession: B22716
A;Molecule type: mRNA
A;Residues: 'V', 50-75, 'S', 76-128 <EDB>
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A;Accession: JJ0005
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A;Cross-references: UNIPARC:UP1000017349C
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
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A; Molecule type: protein
A; Residues: 83, XX, 85-88, XX, 90-108 «KIT»
A; Cross-references: UNIPARC:UP1000017349D
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Molecule type: DNA
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A,Residues: 83-99,'A',101-119 <ZAI>
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US-08-302-069A-12
US-08-302-069A-14
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US-09-576-062A-3
US-09-576-062A-14
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US-09-070-504-17
US-09-576-062A-1
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/jaa/RCOMB.pep:*
/cgn2_6/ptodata/1/jaa/RR_COMB.pep:*
                             GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd
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Maximum Match 100%
Listing first 150 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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84.9%; Score 118; DB 1; I
Best Local Similarity 68.6%; Pred. No. 8.4e-15;
Matches 24; Conservative 0; Mismatches 11;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                            TELEFAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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ANTI-SENSE: NO
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US-08-477-727A-83
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US-08-477-727A-83

Sequence 83, Application US/08477727A

Patent No. 5739106

GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Rink, Timothy
APPLICANT: Peeley, Nigel
APPLICANT: Pricket, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STREET: CA
STREET: CA
COUNTRY: USA
    US-09-576-062A-1

US-09-576-062A-1

US-09-576-062A-11

US-09-576-062A-15

US-09-576-062A-18

US-09-576-062A-18

US-09-454-53-4

US-09-454-533-4

US-09-454-533-12

US-09-454-533-12

US-09-454-533-12

US-09-454-533-22

US-09-454-533-23

US-09-454-533-23

US-09-454-533-23

US-09-454-533-23

US-09-454-533-23

US-09-454-532-14

US-09-454-532-14

US-09-623-548A-321

US-09-623-548A-321

US-09-623-548A-321

US-08-185-185-18

US-08-185-185-18

US-08-185-185-18

US-08-185-185-18

US-08-477-727A-5

US-08-477-727A-10

US-08-454-533-14

US-08-454-533-15

US-08-454-533-15

US-08-454-533-16

US-08-477-727A-10

US-08-454-533-16

US-08-477-727A-10

US-08-454-533-10

US-08-454-533-10

US-08-477-727A-10

US-08-484-533-10

US-08-477-727A-10

US-08-477-727A-10
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US-09-576-062A-5
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-08-259-762-12
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disulfide bridge between the Cys
                                                                                                                      disulfide bridge between the Cyresidues at positions 1 and 6; amidated Tyr at position 36
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OTHER INFORMATION: amidated Tyr at position 36
US-08-471-675A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rolterman, Orville
APPLICANT: Rink, Timothy
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITT: LOS ANGELES
STATE: CA
                                                                                                                                                                                                                                                                                                                                   3 NTATXATORLXNFLXXXXXXXXXXDPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS.
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,675A
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFF, BRADFORD J
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08471675A
Patent No. 5795861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION
TELEPHONE: 619-552-8400
TELEPRAX: 619-552-0157
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68.6%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                 single
                                                                        MOLECULE TYPE: peptide FEATURE:
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                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
         TYPE: am. STRANDEDNESS: BIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
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Pred. No. 8.4e-15;
0; Mismatches 11; Indels
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APPLICANT: Rink, Timothy
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
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COMPUTER: CA
COMPUTER: BABABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATED:
OPERATING SYSTEM: DOS
SOPERATING DATE:
APPLICATION NUMBER: US/08/471,675A
PILING DATE: O5-UN-1995
CLASSIFFICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-193
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 31,048
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08471675A Patent No. 5795861 GENERAL INFORMATION:
FILING DATE:
ATORNEY/AGENT IRFORMATION:
NAME: DUET, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 214/C
TELECPHONE: 619-552-8400
TELEPHONE: 619-552-8400
TELEPHONE: 619-552-0157
TELER:
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68.6%;
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 95 SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.6
Matches 24; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-477-727A-92
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US-08-471-675A-7
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
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Indels
                                                                                                                                                     NS-08-892-549-18
| Sequence 18, Application US/08892549
| Sequence 18, Application US/08892549
| Patent NO. 5998367
| GENERAL INFORMATION:
| APPLICANT: GAETA, Laura S.L. Et Al.
| TITLE OF INVENTION: USES THEREFOR TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 41
| CORRESPONDENCE ADDRESS: ADDRESSE: LYON & LYON
| STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAPTUTE 9001

CAPTUTE FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FILING DATE: 14-JUL-1997
CLASSIFICATION NUMBER: US/08/892,549
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: 00/447,849
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: 07/94,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
RELEPAN: 213/955-0440
11;
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COTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-892-549-18
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                                                                        NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disulfide bridge between
the Cys residues
0; Mismatches
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24; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                          STREET: 633 WEST FICITY: LOS ANGELES STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1,6
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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  Matches
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RESULT 6 US-08-892-549-39

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Sequence 39, Application US/08892549

Sequence 31, Application US/08892549

SERENTIAL OF INVENTION: NORE, AMILIN ACONIES PEPTIDES AND TITLE OF INVENTION: USES TREMEROR WINDS AND SERENTIAL OF UNIVENTION: USES TREMEROR WINDS AND SERENTIAL OF USES AND SECURE OF USES AND SERENTIAL OF USES AND SERENTIAL OF USES AND SEC
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68.6%; Pred. No. 8.4e-15;
tive 0; Mismatches 11; Indels
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ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                      SOFTWARE: Patentin Release #1.0, Verbion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FLING DATE: 07-SEP-1994
CLASSIFICATION NUMBER: 08/18,381
FLING APPLICATION DATE: 07-SEP-1993
ATTONNEY/AGENT INFORMATION:
NAME: DUTT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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OTHER INFORMATION: amidated Tyr (Tyrósinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disulfide bridge between
the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
FILING DATE: 22-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09576062A
Patent No. 6608029
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timchy J.
RINK, Timchy J.
RINK, Timchy J.
RILLE OF INVENTION: METHODS FOR REGULAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3C
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                    213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1,6
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
SPELICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-302-069A-13

Sequence 13, Application US/08302069A

Patent No. 6114304

GENERAL INFORMATION:
APPLICANT: YOUNG Andrew A.
APPLICANT: YOUNG Andrew A.
APPLICANT: RINK, Timothy J.
APPLICANT: BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: AGSTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: disulfide bridge between OTHER INFORMATION: the Cys residues LOCATION: 36 OTHER INFORMATION: amidated Tyr (Tyrosinamide) US-08-302-069A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.9%; Score 118; DB 2;
68.6%; Pred. No. 8.4e-15;
iive 0; Mismatches 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NTATXATQRLXNFLXXXXXXXXCPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 06/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELEPHONE: 619/552-2200
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   ADDRESSER: LYON & LYON STREET: 633 WEST FIFTH STREET CLITY: LOS ANGELES STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear _ WOLECULE TYPE: peptide
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 633 WEST E
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1,6
                                                                                                                                                           90017
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Gaps

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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CORPUTER: IBM PC compatible

APPLICATION DATA:

APPLICATION NUMBER: 08/09/454,533

FILING DATE: CURNOWN-

APPLICATION NUMBER: 07/794,266

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: 07/667,040

FILING DATE: 08-MAR-1991

ATTORNEY/AGENT NUMBER: 08 07/667,040

FILING DATE: 08-MAR-1991

ATTORNEY/AGENT NUMBER: 08 07/667,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09454533
; Patent No. 6610824
; GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                           ; in Location: 36
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-576-062A-13
                                                                                                                                                                                                                                                                                                   Query Match

84.9%; Score 118; DB 2; I
Best Local Similarity 68.6%; Pred. No. 8.4e-15;
Matches 24; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DUFT, BRADFORD J. REGISTRATION NUMBER: 32,219 REFERENCE/DOCKET NUMBER: 227/006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-454-533-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                          ; i.OCATION: 36
; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-576-062A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS FOR REGULATING GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.6%; Pred. No. 8.4e-15; Matches 24; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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CLASSIPICATION: «Unknown»
PRIOR APPLICATION ADTA:
APPLICATION DATA:
FILING DATE: 07-SEP-194
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUTY: BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/55-2200
TELEPHONE: 619/55-0440
                        ATORNEY/AGENT INFORMATION:
NAME: DUFT. BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUTICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
TELEFAX: 213/955-046
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROWN, Kathleen Ann Keiting
            APPLICATION NUMBER: 08/118,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09576062A Patent No. 6608029 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90017
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-576-062A-13
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84.9%; Score 118; DB 1; Length 37; 68.6%; Pred. No. 8.7e-15; tive 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                         ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                           Security Application US/08477727A
Fatent No. 5739106
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Relak, Nigel
APPLICANT: Pricket, Nigel
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 89, Application US/08477727A; Patent No. 5739106; GENERAL INFORMATION: APPLICANT: Rink, Timothy APPLICANT: Young, Andrew APPLICANT: Pricket, Kathryn TILLE OF INVENTION: APPETITE REGULATING; TILLE OF INVENTION: COMPOSITIONS NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 214/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUET, BRADFORD J
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-552-0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                   STATE: CA
COUNTRY: USA
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                   Length 36;
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                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEMTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                   84.9%; Score 118; DB 2;
68.6%; Pred. No. 8.4e-15;
iive 0; Mismatches 11
                                                                                                             3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.9%; Score 118; DB 2;
68.6%; Pred. No. 8.4e-15;
tive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUTT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: LOS ANGELES
                   Query Match
Best Local Similarity 68.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 24; Conserva
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                                                                                                                                                                                                        RESULT 12
US-09-454-533-39
US-09-454-533-18
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Pred. No. 8.7e-15;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
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COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEASESQ VErsion 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATA: 07-JUN-1995
CLASSIPICATION 514
PRIOR APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGGNT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 214/005
TELEPHONE: 619-552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 214/
                                                                                                                                                                                                                                                                                                                                                                                                          91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 68.6'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-477-727A-93
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US-08-477-727A-91

Sequence 91, Application US/08477727A

Patent No. 5739106

GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Rink, Timothy
APPLICANT: Beeley, Nigel
APPLICANT: Pickett, Kathryn
TITLE OF INVENTION: COMPOSITIONS
TITLE OF ANGENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: G33 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
STREET: CA
STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 1;
Pred. No. 8.7e-15;
0; Mismatches 11;
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        CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
                                                                                  CITY: LOS ANGELES
STATE: CA
COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TEASTEN DOS
SOFTWAREN APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 134/005
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 314/005
TELEFPHONE: 619-552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.9%;
68.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 68.69
The 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-477-727A-89
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Gaps

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                                                                                                                            Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues at positions 2 and 7; amidated Tyr at position 37
                                                                                                                         Score 118; DB 1;
Pred. No. 8.7e-15;
0; Mismatches 11.
                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                    3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08471675A
Patent No. 5795861
GENERAL INFORMATION:
APPLICANT: Kolterman, Orville
APPLICANT: Rink, Timothy
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
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68.6%; Pred. No. 8.7e-15;
tive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASELSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,675A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
BEBEDENDER OF COMPRESSIONED STREATS AND 
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                         84.9%;
                                                                                                                         Query Match
Best Local Similarity 68.6 Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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         internal
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MOLECULE TYPE: Peptide
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OTHER INFORMATION:
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CA
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Best Local Similarity
Matches 24, Conserva
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   FRAGMENT TYPE: ;
; ORIGINAL SOURCE: US-08-477-727A-95
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-471-675A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9%; Score 118; DB 1;
68.6%; Pred. No. 8.7e-15;
tive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Voung, Andrew
APPLICANT: Prickett, Kathryn
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDION ILEE.
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/08477727A
Patent No. 5739106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-0400
TELEFAX: 619-552-0157
                                                    TELEX:
INPORMATION FOR EGO ID NO: 9.
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acide
TYPE: amino acide
STRANBEDNESS: single
TOPOLOGY: linear
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.07
Best Local Similarity
Conservative
                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLEGULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
CORIGINAL SOURCE:
US-08-477-727A-93
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LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               internal
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-477-727A-95
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Gaps

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Query Match 84.9%; Score 118; DB 1; Length 37; Best Local Similarity 68.6%; Pred. No. 9.7e-15; Matches 24; Conservative 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08471675A
GENERAL INFORMATION:
APPLICANT: Rolleanch, Orville
APPLICANT: Rolleanch, Orville
APPLICANT: Rink, Timothy
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
COUNTRY: USA
COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
                                                                                          COUNTRY: USA
ZIE: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: OS-JUN-1995
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: UDFT, BRADFORD J
REGISTRATION NUMBER: 213/048
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRAK: 619-552-0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: disulfide bridge between the Cys OTHER INFORMATION: residues at positions 2 and 7; OTHER INFORMATION: amidated Tyr at position 37 US-08-471-675A-13
                                    US-08-471-675A-13

Sequence 13, Application US/08471675A

Sequence 18, Application US/08471675A

Patent No. 5795861

GENERAL INFORMATION:

APPLICANT: Rolterman, Orville
APPLICANT: Rink, Timothy

TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
COUNTRY: USA
ZIP: 90071-2066
COMPUTER: EBM COMPATIBLE
OFERATION SYSTEM: DOS
SOFTWARE: FESTENCE OF STATE:
CAMPUTER: DESCOMPATION OF STATE:
CASSIFICATION NUMBER: US/08/471,675A
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1993
ATPORNEY/AGENT INFORMATION:
PREDERROYE-DOCKET WUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET WUMBER: 213/048
TELEPHONE: 619-552-8400
TELEFRAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
US-08-471-675A-15
; Sequence 15, Application US/08471675A
; Patent No. 5795861
; GENERAL INFORMATION:
; APPLICANT: Kolterman, Orville
APPLICANT: Rink, Timothy
; TITLE OF INVENTION: METHODS FOR REGULATING
; TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXXXXXBXCPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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0; Gaps

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84.9%; Score 118; DB 1; Length 37; 68.6%; Pred. No. 8.7e-15; tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08892549
Patent No. 5998367
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FILING DATE: 14-JUL-1997
CLASSIFICATION S14
PRIOR APPLICATION NUMBER: 08/447,849
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 227/006
TELEPAN: 213/955-0440
TELEPAN: 213/955-0440
TELEPAN: 213/955-0440
TELEPAN: 213/955-0440
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTRISTICS:
SEQUENCE CHARACTRISTICS:
SEGUENTE APALICATION: Acids
                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: disulfide bridge between OTHER INFORMATION: the Cys residues LOCATION: 37 oTHER INFORMATION: amidated Tyr (Tyrosinamide) US-08-892-549-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
  REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                      LOCATION: 2,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90017
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| Sequence 10, Application US/08892549 |
| Sequence 10, Application US/08892549 |
| Patent No. 5998367 |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND |
| TITLE OF INVENTION: USES THEREFOR |
| NUMBER OF SEQUENCES: 41 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: LYON & LYON |
| STREET: 633 WEST FIFTH STREET |
| CITY: LOS ANGELES |
| CITY: LOS ANGELES |
| CALIFORNIA |
| CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disulfide bridge between the Cys residues at positions 2 and 7_i amidated Tyr at position 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FLING DATE: 14-JUL-1997
CLASSIFICATION NUMBER: 08/447,849
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAX-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAX-1991
APPLICATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.9%; Score 118; DB 1;
68.6%; Pred. No. 8.7e-15;
tive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
                   FILING DATE: 05-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATE: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 213/048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
JMBER: US/08/471,675A
05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 68.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-471-675A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
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                                    Length 37;
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                                                                                                                                                                                                                                                                                                             APPLICANT: GAETA, LAURA S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FILING DATE: 14-JUL-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/44,849
FILING DATE: 13-MAY-1995
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION INFORMATION:
NAME: DUET, BRADFORD J:
REGISTRATION NUMBER: 227/006
TELERRAK: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: 37
CTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-892-549-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NIATCATQRLANFLVRSSNNLGPILPSTNVGSNTY 37
                                                                                                                                       Score 118; DB 1;
Pred. No. 8.7e-15;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.9%; Score 118; DB 1;
68.6%; Pred. No. 8.7e-15;
iive 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disulfide bridge between
                                                                                                                3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Cys residues
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 613 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                               US-008-892-549-21
; Sequence 21, Application US/08892549
; Patent No. 5998367
; GENERAL INFORMATION:
                                  Query Match
Best Local Similarity 68.6%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX. 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 aming acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2,7
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90017
US-08-892-549-19
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                                                                                                                                                                                                                     Length 37;
                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
TITLE OF INVENTION: USES THEREFOR
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FILING DATE: 14-JUL-1997
CLASSIFICATION: 514
                                                                              LOCATION: 2,7

OTHER INFORMATION: disulfide bridge between
OTHER INFORMATION: the Cys residues
LOCATION: 37

OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-892-549-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                     84.9%; Score 118; DB 1;
68.6%; Pred. No. 8.7e-15;
iive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                      3 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                   3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disulfide bridge between
the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/447,849
FILING DATE: 23-M2-1995
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 05/667,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADEORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECHANNICATION INFORMATION:
TELECHANNICATION INFORMATION:
TELECHANNICATION INFORMATION:
TELECHANNICATION INFORMATION:
TELECHANNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-892-549-19
; Sequence 19, Application US/08892549
Patent No. 5998367
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELBEAX: 213/>--
TELBEAX: 213/>--
TELBEX: 67-3510
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
STOTEMORY: 37 amino acids
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
    STRANDEDNESS: single
                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: COTHER INFORMATION: t. LOCATION: 37
OTHER INFORMATION: 6
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Best Local Simil
Matches 24; C
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Matches
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84.9%; Score 118; DB 2; Length 37; 68.6%; Pred. No. 8.7e-15; tive 0; Mismatches 11; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
PRIOR APPLICATION NUMBER: 08/118,381
ATONINY/AGENT INPOMBER: 07-SEP-1993
ATONINY/AGENT INPOMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 213/555-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amidated Tyr (Tyrosinamide)
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APPLICANT: YOUNG, Andrew A.
APPLICANT: RINK, Timothy J.
APPLICANT: BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
APPLICANT: RINK, Timothy J.
APPLICANT: BROWN, Kathleen Ann Keiting
APPLICANT: BROWN, METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disulfide bridge between
the Cys residues
                                                                                                                                         ...JUKESSE: LYON & LYON STREET: 633 WEST FIFTH STREET CITY: LOS ANGELES STATE: CALIFORNIA COUNTRY: USA ZIP: 0000-1
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08302069A; Patent No. 6114304; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.64
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                            NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 37
; OTHER INFORMATION: US-08-302-069A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-302-069A-12
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                                                                                                    Sequence 38, Application US/08892549
; Sequence 38, Application US/08892549
; Patent No. 5998367
; GENERAL INFORMATION:
    APPLICANT: GAETA, Laura S.L. Et Al.
    TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 41
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: LYON & LYON
    STREET: GAIN WEST FIFTH STREET
    COUNTRY: USA MUSCLES
    STATE: CALIFORNIA
    COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,549
FLING DATE: 14-JUL-1997
CLASSIFICATION NUMBER: US/08/492,549
FLING DATE: 14-JUL-1997
CLASSIFICATION NUMBER: US/08/492,549
FILING DATE: 13-MAY-1995
APPLICATION NUMBER: 03/47,849
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION INFORMATION:
TELEPHONE: 619/552-2200
TELEPHONE: 619/552-2200
TELEPRASSIFICATION
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OTHER INFORMATION: disulfide bridge between OTHER INFORMATION: the Cys residues LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9%; Score 118; DB 1;
68.6%; Pred. No. 8.7e-15;
iive 0; Mismatches 11;
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Patent No. 6114304
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELBERAX: 213/955 -- TELBERAX: 67-3510
; INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: TWOTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear WOLECULE TYPE: protein
                                                                                                    US-08-892-549-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-892-549-38
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APPLICANT: KOLTERMAN, Orville G. APPLICANT: YOUNG, Andrew A.

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Length 37;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 07-SEP-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 2,7
COTHER INFORMATION: disulfide bridge between
COTHER INFORMATION: the Cys residues
LOCATION: 37
COTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-302-069A-14
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84.9%; Score 118; DB 2; L
Best Local Similarity 68.6%; Pred. No. 8.7e-15;
Matches 24; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOLTERMAN, Orville G.
APPLICANT: YONG, Andrew A.
APPLICANT: YONG, Andrew A.
APPLICANT: RINK, Timothy J.
TITLE OF INVENTION: METHODS FOR REGLIATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
CORRESPONDENCE: 30
CORRESPONDENCE: ADDRESS:
CLASSIFICATION: 51.7

PRIOR APPLICATION DATA:
APPLICATION UNDER: 08/118,381

FILING DATE: 07-5EP-193
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELEPHONE: 619/552-2200
TELEPKX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
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APPLICATION DATA:
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-193
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08302069A, Patent No. 6114304, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90017
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END FC compatible
COMPUTER: THE PC Compatible
COPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN FELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FLING DATE: 07-SEP-1994
CLASSIFICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/POCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE/FOCKET NUMBER: 209/146
TELEFRANCE/FOCKET NUMBER: 21,219
REFERENCE/FOCKET NUMBER: 21,219
RELEFRANCE/FOCKET NUMBER: 21,219
TELEFRANCE/FOCKET NUMBER: 21,219
TELEFRANCE/FOCKET NUMBER: 21,219
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APPLICATION NUMBER: US/08/302,069A FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KOLTERAMN, Orville G.
APPLICANT: KOLTERAMN, Orville G.
APPLICANT: KOUNG, Andrew A.
APPLICANT: HINK, Timothy J.
APPLICANT: BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALLFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: disulfide bridge between OTHER INFORMATION: the Cys residues LOCATION: 37 orther INFORMATION: amidated Tyr (Tyrosinamide) US-08-302-069A-12
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ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
US-08-302-069A-14
F. Sequence 14, Application US/08302069A
Patent No. 6114304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 2,7
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Gaps

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Gaps
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                                                                                                                                                          Length 37;
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                                                                                                                                                                                                   Indels
                      LOCATION: 37
; CTHER INFORMATION: amidated Tyr (Tyrosinamide); SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-576-062A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90017
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOUNG, Andrew A.
RINK, Timochy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
CASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                               3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                        3 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 84.9%; Score 118; DB 2; Best Local Similarity 68.6%; Pred. No. 8.7e-15; Matches 24; Conservative 0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
FILING DATE: 22-May-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 209/146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/302,069
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APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: DUFT, BRADFORD J. REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KOLTERMAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                          US-09-576-062A-12
; Sequence 12, Application US/09576062A
; Patent No. 6608029
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 37 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 213/955-0440
TELEX: 67-3810
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 30
  MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                                                                                                                       RESULT 32
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
FILING DATE: 22-May-2000
CLASSIFCATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                          ch 84.9%; Score 118; DB 2; Length 37; I Similarity 68.6%; Pred. No. 8.7e-15; 24; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                   LOCATION: 2,7
OTHER INFORMATION: disulfide bridge between
OTHER INFORMATION: the Cys residues
LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
US-08-302-069A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GASTROINTESTINAL MOTILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS FOR REGULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09576062A
Patent No. 6608029
GENERAL INPORMATION:
APPLICANT: KOLTERMAN, Orville G.
YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENČE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA COUNTRY: USA
                                                                                      LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
US-09-576-062A-3
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YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                                                                                                                                             ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALLFORNIA
                  APPLICANT: KOLTERMAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                         SEOUENCES:
GENERAL INFORMATION:
                                                                                                                                         NUMBER OF
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US-09-454-533-10
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
FILING DATE: 22-May-2000
CLASSIFCATION SURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                      RINK, Timothy J.
BROWN, Kathleen Ann Keiting
HITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                    3 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 11 18; DB 2; Score 118; DB 2; Conservative 0; Mismatches 11.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEPRAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENČE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                      APPLICANT: KOLTERMAN, Orville G. YOUNG, Andrew A.
                                                                                                                                                        Sequence 14, Application US/09576062A Patent No. 6608029 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ropology: linear
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 37
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Matches 24; Conserve
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US-09-576-062A-16
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                                                                                                                           RESULT 33
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STATE: CALIFORNIA
COUNTY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,062A
FILING DATE: 22-May-2000
CLASSIFICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: UDET, BRADFORD J.
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
REGISTRATION NUMBER: 32,219
TELEPHONE: 619/552-2200
TELEPHONE: 619/552-2200
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Patent No. 6610824

GENERAL INFORMATION

APPLICANT: GAETA, Laura S.L. Et Al.

TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CTHER INFORMATION: amidated Tyr (Tyrosinamide); SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-576-062A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.9%; Score 118; DB 2; 68.6%; Pred. No. 8.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
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; Sequence 16, Application US/09576062A; Patent No. 6608029

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MEDIUM TYPE: Floppy disk
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION NUMBER: 08/892,549
FILING DATE: UNANDATA:
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESUL: 5,
US-09-454-533-19
US-09-454-533-19
; Sequence 19, Application US/09454533
; Patent No. 6610824
; GENERAL INFORMATION:
; APPLICANT: GAETA, Laura S.L. Et Al.
; APPLICANT: GAETA, LOVEL AMYLIN ACONIST PEPTIDES AND TITLE OF INVENTION: USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.9%; Score 118; DB 2; Length 37; ilarity 68.6%; Pred. No. 9.7e-15; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., COTHER INFORMATION: amidated Tyr (Tyrosinamide); SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-454-533-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NTATXATORLXNFLXXXXXXXXXXXXPXTXVGSNTY 37
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/892,549
FILING DATE: -UDKNOWDA:

APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.

REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/667,040 FILING DATE: 08-MAR-1991
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REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                             TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 24; Conserva
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                                                              COMPUTER KEADABLE FURNY

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533

FILING DATE: 06-Dec-1999

CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
APPLICATION NUMBER: 07/794,266

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: 07/794,266

FILING DATE: 19-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: 10FT, BAADFORD J.
REGISTRATION NUMBER: 32,219

REGISTRATION NUMBER: 32,219

REGISTRATION NUMBER: 227/006

TELECOMMUNICATION NUMBER: 227/006

TELEPHONE: 619/552-2200

TELEPHONE: 619/552-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09454533
Patent No. 6610824
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB 2; Length 37
Pred. No. 8.7e-15;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) CTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-454-533-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 37
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FILING DATE: 06-Dec-1999
CLASSIFICATION: <UNKNOWT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
MATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.9%;
                            ZIP: 90017
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 36
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                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09454533
; Patent No. 6610824
; GENERAL INFORMATION:
; APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: USES THEREFOR
                                                                                                                  Length 37;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                   amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.9%; Score 118; DB 2;
68.6%; Pred. No. 8.7e-15;
tive 0; Mismatches 11.
                                                                                                                                                                                                                                  3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
                                                                                                              84.9%; Score 118; DB 2;
68.6%; Pred. No. 9.7e-15;
tive 0; Mismatches 11
                                                                                                                                                                                              3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-D6-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US/07/67,040
FILING DATE: 19-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 227/006
                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-454-533-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: LOS ANGELES STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                           Query Match
Best Local Similarity 68.69
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.6°
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                     US-09-454-533-38
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 06-Dec-1999

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09454533
Sequence 21, Application US/09454533
Patent No. 6610824
GENERAL INPORMATION
GENERAL INPORMATION
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                     Length 37;
                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                       OTHER INFORMATION: amidated Tyr (Tyrosinamide) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                   Score 118; DB 2;
Pred. No. 8.7e-15;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                  3 NTATXATQRLXNFLXXXXXXXXXDXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATCATORLANFLVRSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,549
FILING DATE: «Unknown»
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-NAR-1991
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 227/006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
            TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
                                                     INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                       84.9%;
68.6%;
                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                        LOCATION:
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US-09-454-533-21
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LOS ANGELES
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                                                                                                                 Sequence 11, Application US/08892549
Patent No. 5998367
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 41
CORRESPONDENCES: 41
CORRESPONDENCES: 42
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB 1;
Pred. No. 1.3e-14;
0; Mismatches 11
3 NTATXATQRLXNFLXXXXXXXXXXBXCPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTATCATORIANFLVHRSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disulfide bridge between
the Cys residues
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417,849
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
NAME: DUFT, BRADFORD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,549
FILING DATE: 14-ULL-1997
CLASSIPICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6610824
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/552-2200
TELEFAX: 213/955-0440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1,6
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                   CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity
Matches 24; Conserv;
                                                                                                   US-08-892-549-11
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APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL ANTLIN AGÓNIST PEPTIDES AND
TITLE OF INVENTION: USES THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 36
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
SEQUENCE DESCRIPTION: SEQ ID NO: 116
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

84.2%; Score 117; DB 2;
Best Local Similarity 68.6%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,549
FILING DATE: <unknown>
APPLICATION NUMBER: 07/794,266
FILING DATE: 19-NOV-1991
APPLICATION NUMBER: US 07/667,040
FILING DATE: 08-MAR-1991
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633 WEST FIFTH STREET, SUITE 4700
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APPLICANT: Roung, Andrew
APPLICANT: Beeley, Nigel
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
CORRESPONDENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/454,533 FILING DATE: 06-Dec-1999
                                                                                                 CORRESPONDENČE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 107, Application US/08477727A Patent No. 5739106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                       ZIP: 90017
COMPUTER READABLE FORM:
                                                                                                                                                                            CITY: LOS ANGELES STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                               COUNTRY: USA
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07-SEP-1994

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Sequence 33, Application US/08892549
Sequence 33, Application US/08892549
Fatent No. 599867
GENERAL INFORMATION:
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: disulfide bridge between the Cys OTHER INFORMATION: residues at positions 2 and 7; OTHER INFORMATION: amidated Tyr at position 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUDNIKY: USA

CUNTRY: USA

CIP: 9017

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/892,549

FILING DATE: 14-JUL-1997

CLASSIFICATION: DATA:

APPLICATION NUMBER: 08/44,849

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: 08/794,266

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: US 07/667,040

FILING DATE: 19-NOV-1991

APPLICATION NUMBER: 32,219

REGISTRATION NUMBER: 32,219

REFERENCE/DOCKET NUMBER: 227/006

TELECOMMUTICATION INFORMATION:

NAME: DUFT, BRADFORD J.

REFERENCE/DOCKET NUMBER: 227/006

TELECOMMUTICATION INFORMATION:

MELECOMMUTICATION INFORMATION:

TELECOMMUTICATION INFORMATION:

TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%; Score 117; DB 1;
68.6%; Pred. No. 1.3e-14;
tive 0; Mismatches 11.
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APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 213/048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.64
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213/955-0440
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-892-549-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08471675A
Patent No. 5795861
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
TITLE OF INVENTION: METHODS FOR REGULATING
TITLE OF INVENTION: METHODS FOR REGULATING
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
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STATE: CA
COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,675A
FILING DATE: 05-JUN-1995
                                                                                 MEDIUM ILLE.

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VESTION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER: 32,219
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RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEPAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.6
Matches 24; Conservative
                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
  COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-477-727A-107
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DÓS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/576,062A
FILING BATE: 22-MAY-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 117; DB 2; Length 37;
Pred. No. 1.3e-14;
0; Mismatches 11; Indels
                                                                                                               Length 37;
                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOUNG, Andrew A.
RINK, Timothy J.
BROWN, Kathleen Ann Keiting
TITLE OF INVENTION: METHODS FOR REGULATING
GASTROINTESTINAL MOTILITY
                                                   amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                              3 NTATCATORITNFLVRSSHNLGPALPPTDVGSNTY 37
                                                                                                               84.2%; Score 117; DB 2;
68.6%; Pred. No. 1.3e-14;
tive 0; Mismatches 11
                                                                                                                                                                                                       3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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APPLICATION NUMBER: 08/302,069
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/118,381
FILING DATE: 07-SEP-1993
ATTOKNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J.
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 209/146
TELECOMMUNICATION INFORMATION:
         the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON
STREET: 633 WEST FIFTH STREET
                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09576062A
Patent No. 6608029
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, Orville G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619/552-2200
TELEPAX: 213/955-0440
TELEX: 67-31.0
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: LOS ANGELES STATE: CALIFORNIA
                                                                                                               Query Match
Best Local Similarity 68.61
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.61
Matches 24; Conservative
      OTHER INFORMATION:
                           LOCATION: 37
; OTHER INFORMATION:
US-08-302-069A-28
                                                                                                                                                                                                                                                                                                                                           US-09-576-062A-28
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                                                                                                                                                                                                                                                                                                                                           Length 37;
                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
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APPLICATION DATA:
APPLICATION NUMBER: US/08/302,069A
FILING DATE: 07-SEP-1994
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: 08/118,381
ATTONNEY/AGENT INFORMATION:
NAME: DUET, BRADFORD J.
REGISTRATION NUMBER: 209/146
TELECOMMUNICATION NUMBER: 209/146
TELECOMMUNICATION NUMBER: 209/146
TELECOMMUNICATION NUMBER: 209/146
TELECOMMUNICATION NUMBER: 209/146
TELEFERMENCE/DOCKET NUMBER: 209/146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 45
US-08-302-069A-28
Sequence 28, Application US/08302069A
Sequence 28, Application US/08302069A
Sequence 30, Application US/08302069A
SEQUENCE 30, APPLICANT
SOUNG, Andrew A.
APPLICANT YOUNG, Andrew A.
APPLICANT BROWN, Xathleen Ann Keiting
TITLE OF INVENTION: GASTROINTESTINAL MOTILITY
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON

                                                                                                                                                                                                                                                 LOCATION: 37
OTHER INFORMATION: amidated Tyr (Tyrosinamide)
                                                                                                                                                                                                                                                                                                                                       84.2%; Score 117; DB 1;
68.6%; Pred. No. 1.3e-14;
iive 0; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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OTHER INFORMATION: disulfide bridge between
                                                                                                                                                                                                       disulfide bridge between
                                                                                                                                                                                                                              the Cys residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JO JOHN TESS:
LYON & LYON
LYEET: G13 WEST FIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90017
MPUTUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                           CATION: 2,7
OTHER INFORMATION:
OTHER INFORMATION:
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DB 1; Length 36;
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Fatent No. 5739106
GENERAL INFORMATION:
APPLICANT: Rink, Timothy
APPLICANT: Young, Andrew
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
APPLICANT: Beeley, Nigel
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: APPETITE REGULATING
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 613 WEST FIFTH STREET, SUITE 4700
CITY: LOS ANGELES
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NTATCATORLANFLVRSSNNFGPILPPTNVÖSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 83,5%; Score 116; DB 1; Best Local Similarity 68.6%; Pred. No. 2e-14; Matches 24; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07-JUN-1995
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATOMNEY/AGENT INFORMATION:
NAME: DUFT, BRADFORD J
REGISTRATION NUMBER:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
STATEMENT OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMUNICATION INFORMATION
TELEPHONE: 619-552-8400
TELEPAX: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: 3

CRIGINAL SOURCE: US-08-477-727A-86
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                                                                                                                                                                                                                                                Sequence 33, Application US/09454533
Patent No. 6610824
GENERAL INPORMATION
APPLICANT: GAETA, Laura S.L. Et Al.
TITLE OF INVENTION: NOVEL AMYLIN AGONIST PEPTIDES AND
USES THEREFOR
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84.2%; Score 117; DB 2; Length 37.
Best Local Similarity 68.6%; Pred. No. 1.3e-14;
Matches 24; Conservative 0; Mismatches 11; Indels
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; OTHER INFORMATION: amidated Tyr (Tyrosinamide)
;
US-09-454-533-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/454,533
FILING DATE: 06-Dec-1999
CLASSIFICATION: <Unknown>
                                                                3 NTATCATQRLTNFLVRSSHNLGPALPPTDVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NTATCATORLINFLVRSSHNLGPALPPTDVGSNTY 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 613 WEST PIFTH STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 48
US-08-477-727A-86
; Sequence 86, Application US/08477727A
; Setent No. 5739106
; GENERAL INFORMATION:
; APPLICANT: Rink, Timothy
; APPLICANT: Young, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90017
                                                                                                                                                                                        RESULT 47
US-09-454-533-33
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0; Gaps

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83.5%; Score 116; DB 1; Length 36; 68.6%; Pred. No. 2e-14; tive 0; Mismatches 11; Indels
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Job time : 48 secs
  ATTORNEY/AGENT INFORMATION:
NAME: DUGT, BRADFORD J
REGISTRATION NUMBER: 32,219
REFERENCE/DOCKET NUMBER: 214/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-8400
TELEFAX: 619-552-0157
TELEFAX: 619-552-0167
TELEFAX: 619-652-0167
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acida
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: Amino acid
STRANDEDNESS: single
TYPE: DECULE TYPE: peptide
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE: US-08-477-727A-98
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Pred. No. 2e-14;
0; Mismatches 11; Indels
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US-08-477-727A-98

US-08-477-727A-98

Sequence 99, Application US/08477727A

Sequence 99, Application US/08477727A

Patent No. 5739106

GENERAL INFORMATION:
APPLICANT: Naink, Timothy
APPLICANT: Prickett, Kathryn
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS: 108

COUNTRY: LOS ANGELES

STATE: CA

COUNTRY: LOS ANGELES

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM COMPATI:
COMPATICATION NUMBER: US/08/477,727A

FILING DATE:
CLASSIFICATION NUMBER: US/08/477,727A

FILING DATE:
CLASSIFICATION NUMBER: US/08/477,727A

FILING DATE:
CLASSIFICATION NUMBER: US/08/477,727A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,727A
FILING DATE: 07--UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 314/005
FILING DATE:
APPLICATION NUMBER: 214/005
REGISTRATION NUMBER: 32,219
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEPHONE: 619-552-0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88:
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Best Local Similarity 68.6%;
Matches 24; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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APPLICATION NUMBER:
FILING DATE:
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4.9 37 2 AAR29210 4.9 37 2 AAR29200 4.9 37 2 AAR38812	37 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	37.75	37.7	37.6	, m, c	37 3	37 5	9 37 5 9 37 5	9 37 S 9 37 S	9 37 8 9 37 8	37 B 37 B	37 8	37 8	37 9	9 37 9	9 37 9 9 37 9	37 9	37 8	37 9	100	37.2	2 37 2 2 37 2	37 3	37.5	37 8	37 9	36 2	36 2	36 2	36 2	36 2	36 2	36.2	36 2	5 36 3 AAB1858	386	,
25 118 8 26 118 8 27 118 8 28 118 8	118	111888	118 8	118	118	118	118 8	118 8 118 8	118 8 118 8	118 8 118 8	118 8 118 8	118 8	118 8	118 8	118	118 118 8	118 118 8	118 8	118 8	118 8	117	117 8	117 8	117 8	117 8	117 8	117 8	116 8	116 8	116 8	116 8	116 8	116 8	116 8	116 116 8	116 8	116 8	
5.1.6 Compugen Ltd.		Search time 188 Seconds (without alignments)		TXVGSNTY 37				rs: 2443163										e exect of expects and best	being pr			Description		Aar29201 Des-Lys(1	Aar37789 (Des-Lysi	Aar37787 (des-bys1 Aav22438 Des-bvs1,		Human	Aab18584 Amino aci bah18577 Amino aci	Human	Human	Human	Human	Amylin p	Amylin Human ə	Human	Aar29208 Arg(18)Le Aar29206 Leu(23)Pr Aar29201 Val(26)Pr	
GenCore version 5. Copyright (c) 1993 - 2006 Co	OM protein - protein search, using sw model	Run on: January 4, 2006, 11:29:11 ; Se (wit:	US-09-445-517-14	acore:	Scoring table: BLOSUM62	ממספט י מפספטר מיים	2443163 Seqs, 43	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	ocessing: Minimum Match		Database : A Genesed 21:*	.: :: :: ::	3: geneseqp2000s:* 4: geneseqp2001s:*				ored No is the number of results wreding	greater than or ects derived by analys	•		kesuit No. Score Match Length DB ID	118 84.9 36 2	118 84.9 36 2	118 84.9 36 2	118 84.9 36 2 118 84.9 36 2	118 84.9 36	118 84.9 36 2	118 84.9 36 3	118 84.9 36 5	118 84.9 36 5	118 84.9 36 8	118 84.9 36 8	118 84.9 36 9	118 84.9 36 9 118 84.9 36 9	118 84.9 36 9	22 118 84.9 37 2 AAR29208 23 118 84.9 37 2 AAR29206 24 118 84 9 37 2 AAR29206	

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Treatment of a patient with anorexia or related condition comprises admin. of amylin or an analogue in an amt. sufficient to increase the amylin level in the plasma of the patient. The pref. amylin analogues are given in AAR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt. and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of amylin and opt. insulin for treating anorexia - increases plasma amylin and/or insulin levels, also for treating cachexia conditions,
                                                                                                                                                                                                                                                                                                                  Use of amylin and opt. insulin for treating anorexia - increases plasma amylin and/or insulin levels, also for treating cachexia conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.9%; Score 118; DB 2;
68.6%; Pred. No. 3.6e-14;
iive 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 16; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                adipose tissue deficiency etc.
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                                                                                                                                                                                        (AMYL-) AMYLIN PHARM INC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
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03-APR-1992;
                                                                                                                          24-MAY-1991;
03-APR-1992;
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                                                                               23-MAY-1992;
W09220367-A1
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20-APR-1993
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                                       26-NOV-1992
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Human amy
11e17, Ar
Arg18, Pr
11e17, Le
Pro25, Va
Pro25, Pr
Arg18, Le
11e17, Pr
Human amy
Human amy
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Human amy
Human amy
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Aaw90153
Aaw90158
Aab18586
Aab18593
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Abb05495 Abb05505 Adi36179 Adi36180 Adi36189 Adi36189 Ado51023 Ado51024 Ado51033 Adv92852 Adv92852
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Aar29199 |
Aar29202 |
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Aar36985 I
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Aar3809
Aar37792
Aar37792
Aar37782
Aar3815
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Aaw74607
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AAR36985
AAR38820
AAR38809
AAR37790
AAR37792
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ADD11653
AAW22540
AAW74602
AAW90165
AAY22453
AAY22440
AAY22439
AAY22439
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AAB18586
AAB18593
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AD136180
AD136180
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ADX29205
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AAR29209
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AAY22449
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AAW90158
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(first entry)
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25-MAR-2003 20-APR-1993 AAR29207;

RESULT 1 AAR29207

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Gaps

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be used as hyperglycaemics. The peptide is an analogue of human amylin which mimics the effects of the wild-type hormone. Preferred peptides are used in admixture with insulin for the treatment of diabetes mellitus or with glucagon for the treatment of hypoglycaemic conditions. See AAR37779 and AAR38809-R38826. (Updated on 25-WAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide is an example of amylin agonists of the invention which can be used as hyperglycaemics. The peptide is an analogue of human amylin which mimics the effects of the wild-type hormone. Preferred peptides are used in admixture with insulin for the treatment of diabetes mellitus or with glucagon for the treatment of hypoglycaemic conditions. See AAR37779—R37795 and AAR3809-R38826. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                              Hypoglycaemia; insulin; pancreatic amylòid; diabetes mellitus; glucagon;
hyperglycaemic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
                                                                                                                         Length 36;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                          (Des-Lys1), Arg18, Pro25, Pro28 human amylin analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Arg replaces wild-type His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Pro replaces wild-type Ala"
                                                                                                                                                                             37
                                                                                                                        Score 118; DB 2;
Pred. No. 3.6e-14;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Pro replaces wild-type
                                                                                                                                                                                                     NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY
                                                                                                                                                                              3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 46; Fig 1 and Page 21; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                            AAR37789 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albrecht E;
                                                                                                                        84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-US009842
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones H,
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                                                                                                                                     Local Similarity
nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1992;
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07-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaeta LSL,
                                                                                                                                                                                                                                                                                                       AAR37789;
                                                                                                                           Query Match
                                                                    field.)
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                                                                                                                                        Best Loc
Matches
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                                             Treatment of a patient with anorexia or related condition comprises admin. of amylin or an analogue in an amt. sufficient to increase the amylin level in the plasma of the patient. The pref. amylin analogues are given in AAR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt, and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide is an example of amylin agonists of the invention which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypoglycaemia; insulin; pancreatic amyloid; diabetes mellitus; glucagon;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Des-Lys1), Leu23, Pro25, Val26, Pro28 human amylin analogue.
                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                   Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Pro replaces wild-type Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Pro replaces wild-type Ser"
                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                        Score 118; DB 2;
Pred. No. 3.6e-14;
0; Mismatches 11.
                                                                                                                                                                                                                                                             3 NTATXATQRLXNFLXXXXXXXXXBPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Leu replaces wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Val replaces wild-type
                                                                                                                                                                                                                                                                                      NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 20; Fig 3 and Page 29; 43pp; English
                            Disclosure; Page 16; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ы
                                                                                                                                                                                                                                                                                                                                                             AAR38811 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaeta LSL, Jones H, Albrecht
 adipose tissue deficiency etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00794266.
                                                                                                                                                                                                        84.9%;
68.6%;
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                                                                                                                                                                                                                       Local Similarity 68.6
nes 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperglycaemic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-182488/22
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                                                                                                                                                                              Sequence 36 AA;
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Amylin agonist; human; insulin; diabetes; post-prandial glucose level;
                                                                             Des-Lysl, Argl8, Pro25, Pro28 amylin analogue.
                    AAY22438 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                     (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-458254/38.
                                                                                                              therapy; mutein.
                                                                                                                                                                       Disulfide-bond
Misc-difference
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                 Homo sapiens.
                                                           28-SEP-1999
                                                                                                                                                                                                                                                                                               09-JAN-1998;
                                                                                                                                                                                                                                                                                                                   09-JAN-1998;
                                                                                                                                                                                                                                                       WO9934822-A1
                                                                                                                                                                                                                                                                           15-JUL-1999
                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                            mellitus.
                                        AAY22438;
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          AAY22438
ID AAY2
RESULT 6
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This peptide is an example of amylin agonists of the invention which can be used as hyperglycaemics. The peptide is an analogue of human amylin which mimics the effects of the wild-type hormone. Preferred peptides are used in admixture with insulin for the treatment of diabetes mellitus or with glucagon for the treatment of hypoglycaemic conditions. See AAR37779 -R37795 and AAR38809-R38826. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                               Hypoglycaemia; insulin; pancreatic amyloid; diabetes mellitus; glucagon;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
           Length 36;
           84.9%; Score 118; DB 2; Length 36
68.6%; Pred. No. 3.6e-14;
ive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                    'note= "Pro replaces wild-type Ser"
                                                                                                                                                                                                                                                                                                 "Pro replaces wild-type Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 2;
Pred. No. 3.6e-14;
0; Mismatches 11
                                                  3 NIATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                     NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                             (des-Lys1), Pro25, Pro28-human amylin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Fig 1 and Page 20; 43pp; English.
                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Albrecht E;
                                                                                                                                                                                                                                                                                                                                         /note= "amidated"
                                                                                                                         AAR37787 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US009842
                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00794266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.9%;
Best Local Similarity 68.6%;
Matches 24; Conservative
                                                                                                                                                                           (first entry)
                      l Similarity 68.6
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                 (revised)
                                                                                                                                                                                                                             hyperglycaemic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaeta LSL, Jones H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-182488/22.
                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36 AA;
                                                                                                                                                                                                                                                                             sulfide-bond
                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1992;
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                                                                                                                                                                25-MAR-2003
07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1993
            Query Match
Best Local S
Matches 24
                                                                                                                                             AAR37787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     field.)
                                                                                                                  AAR37787
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98WO-US000288.

Location/Qualifiers

(first entry)

'label= H18R 'label= A25P /label= S28P

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This sequence represents a human amylin analogue, that acts as a amylin agonist. The invention relates to a liquid pharmaceutical formulation (A), that contains (Wt. Vol.): 0.01-0.5% amylin agonist (I); 1-10% carbohydrate or polyol (II); and 0.02-0.5% acetate, phosphate, citrate or glutamate buffer (III); and has pH 3-6. (A) are used, in conjunction with increases in glucose levels of the blood. In these formulations, (I) is stabilised, especially against deamidation and peptide bond hydrolysis for up to 4 years at 5 degrees C amd 30 days at 30 degrees C, without addition of a separate stabiliser. They also retain short-term (up to 24 administered together, reducing the number of information given in the specification
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Stabilized liquid formulation for treatment of insulin-dependent diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 2; I
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NTATXATQRLXNFLXXXXXXXXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY22444 standard; peptide; 36 AA.
                                                                                       Disclosure, Page, 71pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9%;
68.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
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AAY22444
ID AAY2
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Gaps

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Indels

11; 37

NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 36

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3 NTATXATORLXNFLXXXXXXXXXBPXLPXTXVGSNTY

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This invention relates to a method for treating or preventing gastritis or gastric ulceration which comprises administering amylin or an amylin agonist. Amylin administration is not carried out intra-cerebroventricularly. The specification describes a method for treating or preventing a condition for which a non-steroidal anti-inflammatory agent (NSAID) is indicated, comprising administering amylin or amylin agonist, which is not calcitonin, together with NSAID and also a composition comprising an amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat humans by administering it subcutaneously, intravenously or by nasal, orticat pain, fever, inflammation, arthritis, hypercoagulation sequence is an example of an agonist used in the method
                                                                                                                                   non-steroidal anti-inflammatory agent; NSAID; intravenous; subcutaneous; pain; fever; inflammation; arthritis; hypercoagulation.
                                                                           Human amylin agonist peptide des-1-Lys23-Leu25-Pro26-Val28-Pro-amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for treating or preventing gastritis - comprises administering
                                                                                                                Amylin; human; agonist; gastritis; gastric ulceration; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amylin or amylin agonist, except calcitonin
                                                                                                                                                                                                                                                      Location/Qualifiers 1..6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 42; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                             98WO-US009089.
                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00851965.
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                                       15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young A, Gedulin B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-059652/05.
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                                                                                                                                                                                                                                                        Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1998;
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                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                               WO9850059-A1
                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998.
                                                                                                                                                                                                                   Synthetic.
AAW90149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human amylin analogue, that acts as a amylin agonist. The invention relates to a liquid pharmaceutical formulation (A), that contains (Wt./vol.): 0.01-0.5% amylin agonist (I); 1-10% carbohydrate or polyol (III); and 0.02-0.5% acetate, phosphate, citrate or glutamate buffer (III); and has pH 3-6. (A) are used, in conjunction with insulin, for treatment to of diabetes, specifically to reduce post-prandial increases in glucose levels of the blood. In these formulations, (I) is stabilised, especially against deamidation and peptide bond hydrolysis for up to 4 years at 5 degrees C and 30 days at 30 degrees C, without addition of a separate stabiliser. They also retain short-term (up to 24 min stability when combined with insulin, allowing both agents to be administered together, reducing the number of injections required. Note: This sequence was created by the indexer from information given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stabilized liquid formulation for treatment of insulin-dependent diabetes
                                                                                                                                     Amylin agonist; human; insulin; diabetes; post-prandial glucose level;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                              Des-Lys1, Leu23, Pro25, Val26, Pro28 amylin analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB 2; L
Pred. No. 3.6e-14;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruby C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 71pp; English.
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68.6%;
                                                                                                                                                                                                                                                                                                                    /label= F23L
                                                                                                                                                                                                                                                                                                                                                      label= A25P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US000288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US000288
                                                                                                                                                                                                                                                                                                                                                                                             'label= 126V
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= S28P
                                                       28-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L'italian J, Musunuri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 68.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                             9. ..
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                                                                                                                                                                                                                                                                                                                                    Misc-difference 2
                                                                                                                                                            therapy; mutein.
                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 AA;
                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9934822-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999
                                                                                                                                                                                                                   Synthetic.
                  AAY22444;
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                                                Gaps
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                  Human amylin agonist peptide des-1-Lys18-Arg25,28-Pro-amylin.
    Length 36;
                                              Indels
Score 118; DB 2;
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                        37
                                                                                                                                    2 NTATCATÓRLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                            3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                   AAW90141 standard; peptide; 36 AA
    84.9%;
68.6%;
                                                                                                                                                                                                                                                                                                                                         15-MAR-1999 (first entry)
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AAW90149 standard; peptide; 36 AA.

AAW90149 ID AAW9 XX RESULT 8

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/note= "amidated residue"
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1994;
                                                                       07-SEP-1994;
                                                                                             07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6114304-A.
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                         US6114304-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB18577;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
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    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for treating or preventing gastritis or gastric ulceration which comprises administering amylin or an amylin agonist. Amylin administration is not carried out intra-cerebroventricularly. The specification describes a method for treating or preventing a condition for which a non-steroidal anti-inflammatory agent (NSAID) is indicated, comprising administering amylin or amylin composition comprising an amylin or an amylin agonist, which is not calcitonin, together with NSAID and also a composition comprising an amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is used to treat humans by administering it subcutaneously, intravenously or by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat pain, fever, inflammation, arthritis, hypercoagulation and other condition where an NSAID would be indicated. The present sequence is an example of an agonist used in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycenta; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
                                                                                                                                                                                                                                                          Method for treating or preventing gastritis - comprises administering amylin or amylin agonist, except calcitonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of an amylin agonist analogue compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
   pain; fever; inflammation; arthritis; hypercoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 84.9%; Score 118; DB 2; 11 Similarity 68.6%; Pred. No. 3.6e-14; 24; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                          Location/Qualifiers
1. .6
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                                                                                                                                                                                                                Beynon GW;
                                                                                                                                                                                                                                                                                                Claim 6; Page 42; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18584 standard; peptide; 36
                                                                                                                                             98WO-US009089
                                                                                                                                                                   97US-00851965.
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                                                                                                                                                                                         (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.
                                                                                                                                                                                                                 Gedulin B,
                                                                                                                                                                                                                                       WPI; 1999-059652/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
Modified-site
                                                                        Digulfide-bond
                           Homo sapiens
                                                                                               WO9850059-A1
                                                                                                                                             06-MAY-1998;
                                                                                                                                                                    06-MAY-1997;
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                                                                                                                      12-NOV-1998
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                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB18584;
                                                                                                                                                                                                                 Young A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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      FIFE
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The present sequence represents an amylin agonist analogue compound. Amylin or amylin agonists are administered for reducing gastric motility or delaying gastric emptying, and for treating postprandial dumping syndrome or postprandial hypersylvemia, by inducing amylin activity, in a mammal. The peptides are used to reduce gastric motility or for delaying pastric emptying in a mammal undergoing gastrointestinal diagnostic procedures, such as radiological examination or magnetic resonance imaging. They are also used for reducing gastric motility in agastrointestinal disorder, especially spass, which is associated with a disorder of acute diverticulitie or disorders of biliary tract or sphincter of oddi. They are also used to treat postprandial dumping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                 Treating gastrointestinal disorder e.g. spasm by reducing gastric motility or delaying gastric emptying, postprandial dumping syndrome or postprandial hyperglycemia, by administering amylin or amylin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.9%; Score 118; DB 3;
68.6%; Pred. No. 3.6e-14;
cive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                 Kolterman OG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome or postprandial hyperglycemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 43-44; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .6
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                                                                                                                                                                                                                     Young AA, Rink TJ, Brown KAK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB18577 standard; peptide; 36
94US-00302069
                                                                   93US-00118381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                              (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                        WPI; 2000-601336/57
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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ID ABB(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                     The present sequence represents an amylin agonist analogue compound. Amylin or amylin agonists are administered for reducing gastric motility or delaying gastric emptying, and for treating postprandial dumping syndrome or postprandial hyperglycemia, by inducing amylin activity, in a mammal. The peptides are used to reduce gastric motility or for delaying gastric emptying in a mammal undergoing gastrointestinal diagnostic procedures, such as radiological examination or magnetic resonance imaging. They are also used for reducing gastric motility in gastrointestinal disorder, especially spasm, which is associated with a disorder of acute diverticulities or disorders of biliary tract or sphincter of oddi. They are also used to treat postprandial dumping syndrome or postprandial hyperglycemia
                                                                                                                                                                                                                                                                                                                                                                          in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pharmaceutical formulation useful for treating patients with type II
                                                                                                                                                                                                          or
                                                                                                                                                                                Treating gastrointestinal disorder e.g. spasm by reducing gastric
motility or delaying gastric emptying, postprandial dumping syndrome or
postprandial hyperglycemia, by administering amylin or amylin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate;
liquid pharmaceutical formulation; polyhydric alcohol; phosphate;
citrate; glutamate; buffer; antidiabetic; type II diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human amylin agonist des-1Lys23Leu25Pro26Val28Pro-h-amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.9%; Score 118; DB 3;
68.6%; Pred. No. 3.6e-14;
iive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
                                                                                                     Kolterman OG;
                                                                                                                                                                                                                                                                    Disclosure; Col 39-40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB05499 standard; peptide; 36 AA
                                                                                                     Brown KAK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruby
                   93US-00118381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 68.6
24; Conservative
                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L'italien J, Musunuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L'ITALIEN J.
MUSUNURI S.
                                                                                                   Rink TJ,
                                                                                                                                         WPI; 2000-601336/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-163554/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RUBY K.
                   07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2002
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                                                                                                     Young AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB05499;
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ABB05499
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comprising (wt/vol*) an amylin agoinst (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or alcohol (1 - 10) and an acetate, phosphate, citrate or glutamate buffer (0.02 - 0.5) having a ph of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comprises a borosilicate glass vial having an open end, a stopper for multiuse comparible with the amylin and/or amylin agoinst tixed in the open end of the vial. The package also comprises a cartridge for use in a pen injector. (A) has antidiabetic activity and can be used in the treatment of patients with type II diabetes. The formulation comprises amylin agoinst which is biologically active, has a reduced tendency to form aggregates in water or at a pressure of greater than 2 psi and has a reduced tendency to precipitate in the presence of NaCl compared to human amylin. The formulation maintains stability upon storage under refrigerated or room-température conditions. The formulation retains short-term mixing compatibility with insulin and results in improved stability of the hormone and the patients no longer need to refrigerate the vial of insulin in use. The present sequence represents a human amylin peptide analogue, which can be used as an amylin agonist in the present invention. N.B. The present sequence is not given in the present specification but is derived from the 37 amino acid human amylin as stated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
diabetes comprises amylin agonist, carbòhydrate or polyhydric alcohol and
a buffer.
                                                                                                                                                                                           The present invention describes a liquid pharmaceutical formulation (A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human amylin agonist des-1Lys18Arg25,28Pro-h-amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 5;
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
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                                                                                                                  Disclosure; Page; 19pp; English
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Best Local Similarity 68.6%;
Matches 24; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LITA/) L'ITALIEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-163554/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2001043934-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RUBY/) RUBY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39-JAN-1998;
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ADI36183;
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  8XCCCCCCCXXXX535CCC
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                                                                              comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a collumnate buffer (0.02 - 0.5) having a ph of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comprisible with the amylin and/or amylin agonist cropper for multiuse compatible with the amylin and/or amylin agonist cropper in the far end of the vial and an aluminium band to retain the cropper in the far end of the vial. The package also comprises a carridge for use in a pen injector. (A) has antidiabetes. The crompatein comprises amylin agonist which is biologically active, has a carridge for use in a pen injector. (A) has antidiabetes of greater comparises amylin agonist which is biologically active, has a reduced tendency to precipitate in the presence of formulation comprises amylin agonist which is biologically active, has a reduced tendency to precipitate in the presence of than 2 psi and has a reduced tendency to precipitate in the presence of storage under refrigerated or room-temperature conditions. The compared to human amylin, the formulation maintains stability upon storage under refrigerate the vial of insulin in use. The present sequence is not crepresents a human amylin persent invention.

C human amylin as stated in the invention
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patients with type II polyhydric alcohol and
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                        present invention describes a liquid pharmaceutical formulation
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                                                                                                                                                                                                                                                                                                                                                                                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keating Brown KA;
  New pharmaceutical formulation useful for treating diabetes comprises amylin agonist, carbohydrate or
                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 5;
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amidated tyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI36176 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human amylin agonist anologue #5.
                                                    Disclosure, Page, 19pp, English
                                                                                                                                                                                                                                                                                                                                                                                          84.9%;
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94US-00302069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
Modified-site
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07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                     The present invention is directed to novel methods for reducing gastric motility and delaying gastric emptying, comprising the administration of an amylin or an amylin agonist. The invention is useful for reducing gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes. The invention is also useful for treating conditions associated with elevated, inappropriate or undesired post-prandial blood glucose levels and treating ingestion of a toxin. The present sequence is human amylin agonist analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing gastric motility or delaying gastric emptying in a mammal, useful for treating post-prandial hyperglycemia, comprises administering an amylin or an amylin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is directed to novel methods for reducing gastric motility and delaying gastric emptying, comprising the administration of an amylin or an amylin agonist. The invention is useful for reducing
                                              Reducing gastric motility or delaying gastric emptying in a mammal, useful for treating post-prandial hyperglycemia, comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gastric motility; gastric emptying; amylin agonist; therapy; diagnosis; antidiabetic; hypoglycaemia; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.9%; Score 118; DB 8;
68.6%; Pred. No. 3.6e-14;
tive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXXXXXXX37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY 36
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                                                                                                                                                                  Disclosure; SEQ ID NO 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI36183 standard; peptide; 36 AA
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                                                                                                           an amylin or an amylin agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-2004 (first entry)
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WPI; 2004-118064/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 AA;
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Modified-site
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07-SEP-1994;
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invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is directed to novel methods for reducing gastric motility and delaying gastric emptying which comprises the administration of an amylin or an amylin agonist. The invention is useful for treating postprandial dumping syndrome, postprandial hyperglycemia and reducing gastric motility associated with gastrointestinal disorders such as spasm or delaying gastric emptying in a mammal undergoing a gastrointestinal disorders such as radiological examination and magnetic resonance imaging. The invention is also useful for lowering postprandial blood glucose levels during treatment of diabetes. The present sequence is human amylin agonist peptide analogue. This sequence is used in the
gastric motility and delaying gastric emptying for therapeutic and diagnostic purposes. The invention is also useful for treating conditions associated with elevated, inappropriate or undesired post-prandial blood glucose levels and treating ingestion of a toxin. The present sequence is human amylin agonist analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of amylin agonist for reducing gastric motility, delaying gastric emptying and for treating postprandial dumping syndrome and postprandial hyperglycemia.
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                           postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal disorder; spasm; radiological examination; magnetic resonance imaging; diabetes; therapy; human.
                                                                                                                                                                                                                                                                                                                  Gastric motility; delay gastric emptying; amylin; agonist;
                                                                                            Length 36;
                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keating Brown KA;
                                                                                           Score 118; DB 8;
Pred. No. 3.6e-14;
                                                                                                                                        3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                             NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                          Human amylin agonist peptide analogue #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rink TJ,
                                                                                                                                                                                                                      ADO51020 standard; peptide; 36 AA
                                                                                        84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1993; 93US-00118381.
07-SEP-1994; 94US-00302069.
22-MAY-2000; 2000US-00576062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-2003; 2003US-00643681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEATING BROWN K A.
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                   24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kolterman OG, Young AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KOLT/) KOLTERMAN O G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-389180/36
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOUNG A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      כי
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                                                                     Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RINK T
                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                    18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BROW/)
                                                                                                                   Matches
                                                                                                                                                                                                 RESULT 16
                                                                                                                                                                                                             ADO51020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of amylin agonist for reducing gastric motility, delaying gastric emptying and for treating postprandial dumping syndrome and postprandial hyperglycemia.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gastric motility, delay gastric emptying; amylin; agonist; postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal disorder; spasm; radiological examination; magnetic resonance imaging; diabetes; therapy; human.
                                                    Length 36;
                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young AA, Rink TJ, Keating Brown KA;
                                                    Score 118; DB 8;
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                                                                                                      3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                             2 NTATCATORLANFLVRSSNNFGPILPSTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human amylin agonist peptide analogue #13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              ADO51027 standard; peptide; 36 AA
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22-MAY-2000; 2000US-00576062.
                                                    84.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2004 (first entry)
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(BROW/) KEATING BROWN K A.
                                                    Query Match
Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOLTERMAN O G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-389180/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004097415-A1
Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO51027;
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18-NOV-2004; 2004US-00991597.
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                                                                                                         WO2005000222-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
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                                                                                                                                              06-JAN-2005
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Matches
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AEB17945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a pharmaceutical composition for transmucosal administration of a bioactive peptide/protein (e.g. exendin, PYY, GLP-1 or amylin peptide/protein) of interest. The composition of the invention is useful for the transmucosal administration of a bioactive peptide or protein and is useful for treating or preventing viral or bacterial diseases in humans. The present amino acid sequence represents an amylin peptide that is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                            delivery mechanism; viral infections; virucide; bacterial infection;
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   Length 36;
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                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 36
Score 118; DB 8;
Pred. No. 3.6e-14;
0; Mismatches 11.
                                                                        NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 36
                                                                                                                                                                                                                                                                                                                        Amylin peptide amino acid sequence - SEQ ID 287
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Pred. No. 3.6e-14;
0; Mismatches 11
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   84.9%;
                     68.68;
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                                                                                                                                                                                                                                                                                     (first entry
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                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; amylin.
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les 24; Conserv
                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                       24-MAR-2005
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Best Local Si
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Query Match
Best Local 6
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AAC ADV9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a pharmaceutical composition for transmucosal administration of a bioactive peptide/protein (e.g. exendin, PYY, GLP-1 or amylin peptide/protein) of interest. The composition of the invention is useful for the transmucosal administration of a bioactive peptide or protein and is useful for treating or preventing viral or bacterial diseases in humans. The present amino acid sequence represents an amylin peptide that is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
mechanism; viral infections; virucide; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.9%; Score 118; DB 9;
68.6%; Pred. No. 3.6e-14;
iive 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATXATORLXNFLXXXXXXXXXXPXLPXTXVGSNTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jennings R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB17945 standard; peptide; 36
                                                                                                                                                                                                                                                                                    28-MAY-2004; 2004WO-US017456
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                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC.
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      delivery mechanism; vi
antibacterial; amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stetsko G,
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Treatment of a patient with anorexia or related condition comprises admin. of amylin or an analogue in an after. sufficient to increase the amylin level in the plasma of the patient. The pref. amylin analogues are given in AAR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt. and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-
             New transmucosal glucose-regulating peptide (GRP) formulation, useful for treating e.g. obesity, hyperglycemia, dyslipidemia and diabetes mellitus and for inducing satiety in an individual and to promote weight-loss in
                                                                                                                                          comprising at least one glucose regularing peptide (GRP) such as amylin, an amylin analog (such as pramlintide), glucagon-like peptide-1 (GLP)-1, exendin-3 or exendin-4 and one or more mucosal delivery-enhancing agents. The formulation or the method is useful for treating variety of diseases and conditions in mammalian subjects including obesity, hyperglycemia, dyslipidemia and diabetes mellitus and for inducing satiety in an individual and to promote weight-loss in an individual. The invention is also useful in protein therapy. The present sequence is the human pramlintide peptide, which serves as an amylin agonist peptide.
                                                                                                                          present invention relates to pharmaceutical compositions and methods orising at least one glucose regulating peptide (GRP) such as amylin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of amylin and opt. insulin for treating anorexia - increases pla amylin and/or insulin levels, also for treating cachexia conditions, adipose tissue deficiency etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arg(18)Leu(23)Pro(25)Val(26)Pro(28)-h-amylin for treating anorexia.
                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                           84.9%; Score 118; DB 9;
68.6%; Pred. No. 3.6e-14;
ive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                              2 NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                             3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY
                                                                                            Claim 7; SEQ ID NO 44; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anorexia; cachexia; adipose; amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 16; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR29208 standard; protein; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00704995.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
                                               and for induc
an individual
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20-APR-1993
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                                                                                                                                          New transmucosal glucose-regulating peptide (GRP) formulation, useful for treating e.g. obesity, hyperglycemia, dyslipidemia and diabetes mellitus and for inducing satiety in an individual and to promote weight-loss in
                                                                                                                                                                                                                                                         The present invention relates to pharmaceutical compositions and methods comprising at least one glucose regulating peptide (GRP) such as amylin, an amylin analog (such as pramlintide), glucagon-like peptide-1 (GLP)-1, exendin-3 or exendin-4 and one or more mucosal delivery-enhancing agents. The formulation or the method is useful for treating variety of diseases and conditions in mammalian subjects including obesity, hyperglycemia, dyslipidemia and diabetes mellitus and for inducing satiety in an individual and to promote weight-loss in an individual. The invention is also useful in protein therapy. The present sequence is the human pramilitide peptide, which serves as an amylin agonist peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pharmaceutical; weight loss; obesity; anorectic; nutritional disorder; hyperglycemia; antidiabetic; metabolic disorder; antilipemic; diabetes mellitus; metabolic disorder; glucose regulating peptide; amylin agonist; pramilintide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 9;
Pred. No. 3.6e-14;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; SEQ ID NO 23; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.9%;
             26-DEC-2003; 2003US-0532337P.
                                              (NAST-) NASTECH PHARM CO INC
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                                                                              Costantino HR;
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                                                                                                             WPI; 2005-496434/50
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
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an individual
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                                                                            Quay SC,
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Sequence 37 AA;
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03-APR-1992;
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20-APR-1993
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20-APR-1993
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AAR29203;
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                                                                                                                                                                                                   Leu(23)Pro(25)Val(26)Pro(28)-h-amylin for treating anorexia.
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                                    Length 37;
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                                   84.9%; Score 118; DB 2;
68.6%; Pred. No. 3.7e-14;
iive 0; Mismatches 11;
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                                                                                  NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                       3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY
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                                                                                                                                       AAR29206 standard; protein; 37
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92US-00862500
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(first entry)
  2003 to correct PN field.)
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nes 24; Conservative
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nes 24; Conserv
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20-APR-1993
                   Sequence 37
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Matches
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Treatment of a patient with anorexia or related condition comprises admin. Of amylin or an analogue in an amt. sufficient to increase the amylin level in the plasma of the patient. The pref. amylin analogues are given in AAR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt. and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                              Val(26)Pro(25,28)-h-amylin for treating anorexia.
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68.6%; Pred. No. 3.7e-14;
iive 0; Mismatches 11
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                                                                                                                                     Anorexia; cachexia; adipose; amylin
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92US-00862500.
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                          (first entry)
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(revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young AA;
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amylin level in the plasma of the patient. The pref. amylin analogues are given in AAR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt. and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This peptide is an example of amylin agonists of the invention which can be used as hyperglycaemics. The peptide is an analogue of human amylin which mimics the effects of the wild-type hormone. Preferred peptides are used in admixture with insulin for the treatment of diabetes mellitus or with glucagon for the treatment of hypoglycaemic conditions. See AAR37779-R37795 and AAR18809-R38826. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                               Hypoglycaemia; insulin; pancreatic amyloid; diabetes mellitus; glucagon;
hyperglycaemic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used for treatment and prevention of
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                                                                                                                        Length 37;
                                                                                                                                                    Indels
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Misc-difference 28
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                                                                                                                        Score 118; DB 2;
Pred. No. 3.7e-14;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypoglycaemia and diabetes mellitus.
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                                                                                                                     Local Similarity 68.6%;
les 24; Conservative 0
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                                                                                                Sequence 37 AA;
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                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
07-SEP-1993
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                                                                                                                                                                                                                                                                                                         AAR37786;
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                                                                                                                           Query Match
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                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                   RESULT 27
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                                                                                                                                                                                                                   admin. of amylin or an analogue in an amt. sufficient to increase the amylin level in the plasma of the patient. The pref. amylin analogues are given in AR29197-222. Treating a patient deficient in adipose tissue comprises admin. of amylin or an analogue and/or insulin in an amt. and ratio sufficient to increase adipose tissue. Typical dosage units contain 0.1-10 mg of amylin analogue and 0.1-1 mg of insulin. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                       Use of amylin and opt. insulin for treating anorexia - increases plasma amylin and/or insulin levels, also for treating cachexia conditions, adipose tissue deficiency etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating anorexia - increases plasma for treating cachexia conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of a patient with anorexia or related condition comprises admin. of amylin or an analogue in an amt. sufficient to increase the
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                          Freatment of a patient with anorexia or related condition comprises
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                             84.9%; Score 118; DB 2; Length 37; 68.6%; Pred. No. 3.7e-14; ive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arg(18) Pro(25,28) -h-amylin for treating anorexia.
                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                     Anorexia; cachexia; adipose; amylin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of amylin and opt. insulin for amylin and/or insulin levels, also adipose tissue deficiency etc.
                                                                                                                                                                              Disclosure; Page 16; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 16; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR29200 standard; protein; 37 AA
 91US-00704995
92US-00862500
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(first entry)
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                                         (AMYL-) AMYLIN PHARM INC
                                                                                              WPI; 1992-415470/50.
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                                                                   Rink TJ, Young AA;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                     Sequence 37 AA;
 24-MAY-1991;
03-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9220367-A1
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20-APR-1993
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Best Local S
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Matches
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Hypoglycaemia;
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                 27-MAY-1993
                                                                                    25-MAR-2003
07-SEP-1993
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                                                                    AAR38814;
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                                                                                                                                                               insulin; pancreatic amyloid; diabetes mellitus; glucagon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
             Gaps
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             Indels
                                                                                                                                              Arg18, Leu23, Pro25, Val26, Pro28 human amylin analogue
                                                                                                                                                                                                                               note= "Arg replaces wild-type His"
                                                                                                                                                                                                                                                                                  note= "Val replaces wild-type Ile"
                                                                                                                                                                                                                                                                                                   'note= "Pro replaces wild-type Ser"
Pred. No. 3.7e-14;
                            NTATXATQRLXNFLXXXXXXXXXXXXPXTXVGSNTY 37
                                       NTATCATORLANFLVHSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                 note= "Leu replaces wild-type
                                                                                                                                                                                                                                                                 note= "Pro replaces wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 21; Fig 3 and Page 29; 43pp; English.
                                                                                                                                                                                                  Location/Qualifiers 2...7
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                                                                                                                                                                                                                                                                                                                   /note= "amidated"
                                                                                      AAR38812 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                     Albrecht
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   68.68;
                                                                                                                               (first entry)
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (AMYL-) AMYLIN PHARM INC
                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                     Jones H,
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-182488/22.
     Similarity
                                                                                                                                                                                                                Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37 AA;
                                                                                                                                                                Hypoglycaemia;
hyperglycaemic
                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1991;
                                                                                                                                                                                         Homo sapiens
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                                                                                                                       25-MAR-2003
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                                                                                                                               07-SEP-1993
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                                                                                                        AAR38812;
     Best Local
             Matches
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                                                                                                                                                                                insulin; pancreatic amyloid; diabetes mellitus; glucagon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                           /note= "Arg replaces wild-type His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 2; I
Pred. No. 3.7e-14;
0; Mismatches 11;
                                                                                                                                           Arg18, Leu23, Pro25, Pro28-human amylin analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 23; Fig 3 and Page 29; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Pro replaces
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "amidated"
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AAR38814 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US009842.
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                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
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                                                                                                                                                                                                             agent
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                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 23
                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                     Misc-difference
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11arity 68.6%; Score 118; DB 2; 11arity 68.6%; Pred. No. 3.7e-14; Conservative 0; Mismatches 11;

Best Local Similarity Matches 24; Conserv

Query Match

RESULT 30 AAR37788

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Gaps

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Length 37; 11; Indels

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This peptide is an example of amylin agonists of the invention which can be used as hyperglycaemics. The peptide is an analogue of human amylin which mimics the effects of the wild-type hormone. Preferred peptides are used in admixture with insulin for the treatment of diabetes mellitus or with glucagon for the treatment of hypoglycaemic conditions. See AAR37779-R37795 and AAR3809-R38826. (Updated on 25-MAR-2003 to correct PN
 Hypoglycaemia; insulin; pancreatic amyloid; diabetes mellitus; glucagon;
hyperglycaemic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amylin agonist; human; insulin; diabetes; post-prandial glucose level; therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New amylin agonist peptide(s) - used for treatment and prevention of hypoglycaemia and diabetes mellitus.
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Pred. No. 3.7e-14;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NTATXATQRLXNFLXXXXXXXXXXXXX37
                                                                                                                                    note= "Leu replaces wild-type
                                                                                                                                                                  'note= ."Pro replaces wild-type
                                                                                                                                                                                                                              /note= "Pro replaces wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 19; Fig 3 and Page 29; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leu23, Pro25, Val26, Pro28 amylin analogue.
                                                                                                                                                                                                'note= "Val replaces
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY22443 standard; peptide; 37 AA
                                                                                                                                                                                                                                                           /note= "amidated"
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les 24; Conserv
                                                                                                                                                   Misc-difference 25
                                                                                                                                                                               Misc-difference 26
                                                                                                     Disulfide-bond
Misc-difference
                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                             Modified-site
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Synthetic.
                                                              Homo sapiens
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Matches
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                                                                                                                               Hypoglycaemia; insulin; pancreatic amyloid; diabetes mellitus; glucagon; hyperglycaemic agent.
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                                                                                                                                                                                                                                                            note= "Arg replaces wild-type His"
                                                                                                                                                                                                                                                                                        note= "Pro replaces wild-type Ala"
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68.6%; Pred. No. 3.7e-14;
iive 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                       note= "Pro replaces wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 45; Fig 1 and Page 20; 43pp; English.
                                                                                                         Arg18, Pro25, Pro28 human amylin analogue.
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AAR37788 standard; peptide; 37
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                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-182488/22.
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                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 AA;
                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1991;
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 WO9310146-A1
                                                          25-MAR-2003
07-SEP-1993
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07-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaeta LSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR38810;
                               AAR37788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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ID AAR3
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DT 25-M
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Gaps

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label= A25P

label= H18R

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Misc-difference 25
                                     Misc-difference 23
Disulfide-bond
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                      mellitus
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                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a human amylin analogue, that acts as a amylin agonist. The invention relates to a liquid pharmaceutical formulation (A), that contains (wr./vol.): 0.01-0.5% amylin agonist (I); 1-10% carbohydrate or polyol (II); and has pH 3-6. (A) are used, in conjunction with sinciases in glucoae levels of the blood. In these formulations, (I) is stabilised, especially against deamidation and peptide bond hydrolysis for up to 4 years at 5 degrees C and 30 days at 30 degrees C, without addition of a separate stabiliser. They also retain short-term (up to 24 hr) stability when combined with insulin, allowing both agents to be administered together, reducing the number of injections required. Note:
                                                                                                                                                                                                                                                                                                               Stabilized liquid formulation for treatment of insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amylin agonist; human; insulin; diabetes; post-prandial glucose level;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arg18, Leu23, Pro25, Val26, Pro28 amylin analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 2;
Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTATCATORLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
   Location/Qualifiers
                                                                                                                                                                                                                                                                 Ruby C;
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                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY22445 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.9%;
68.6%;
                                                                                                                                                                                         98WO-US000288
                                                                                                                                                                                                                98WO-US000288
                                       label= F23L
                                                                label= A25P
                                                                                                                 /label= S28P
                                                                                        label= I26V
                                                                                                                                                                                                                                                                 Musunuri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 68.6
                                                                                                                                                                                                                                        (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                         WPI; 1999-458254/38.
                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; mutein.
                                                   Misc-difference
                             Misc-difference
                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 AA;
                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                 L'italian J,
                                                                                                                                                                                         09-JAN-1998;
                                                                                                                                                                                                                 09-JAN-1998;
                                                                                                                                         W09934822-A1
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Matches
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This sequence represents a human amylin analogue, that acts as a amylin agonist. The invention relates to a liquid pharmaceutical formulation caponist. The invention relates to a liquid pharmaceutical formulation (A), that contains (wt./vol.): 0.01-0.5% amylin agonist (I); 1-10% carbohydrate or polyol (II); and 0.02-0.5% acetate, phosphate, citrate or glutamate buffer (III); and has pH 3-6. (A) are used, in conjunction with consulin, for treatment of diabetes, specifically to reduce post-prandial correspens in glucose levels of the blood. In these formulations, (I) is stabilised, especially against deamidation and peptide bond hydrolysis of for up to 4 years at 5 degrees C amd 30 days at 30 degrees C, without addition of a separate stabiliser. They also retain short-term (up to 24 administered together, reducing the number of injections required. Note: This sequence was created by the indexer from information given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stabilized liquid formulation for treatment of insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amylin agonist; human; insulin; diabetes; post-prandial glucose level;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.9%; Score 118; DB 2; I
68.6%; Pred. No. 3.7e-14;
ive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NTATCATORLANFLVRSSNNLGPVLPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arg18, Pro25, Pro28 amylin analogue.
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                                                                                                                                                                                                                                                                                     98WO-US000288.
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                                                                                           /label= S28P
                             /label= I26V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-458254/38.
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Misc-difference 26
                                                              Misc-difference 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
Synthetic.
                                                                                                                                                                                                                                                                                     09-JAN-1998;
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/label= H18R

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Misc-difference
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                                                                                                                                                                                                                             mellitus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                   agonist. The invention relates to a liquid pharmaceutical formulation carbohydrate or polyol (II); and 0.02-0.5% amplin agonist (II); 1-10% carbohydrate or polyol (II); and 0.02-0.5% acctate, phosphate, citrate or glutamate buffer (III); and has pH 3-6. (A) are used, in conjunction with insulin, for treatment of diabetes, specifically to reduce post-prandial increases in glucose levels of the blood. In these formulations, (I) is stabilised, especially against deamdation and peptide bond hydrolysis for up to 4 years at 5 degrees C and 30 days at 30 degrees C, without hr) stability when combined with insulin, allowing both agents to be administered together, reducing the number of injections required. Note: This sequence was created by the indexer from information given in the
                                                                                                                                                                                                                            Stabilized liquid formulation for treatment of insulin-dependent diabetes
                                                                                                                                                                                                                                                                         sequence represents a human amylin analogue, that acts as a amylin ist. The invention relates to a liquid pharmaceutical formulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amylin agonist; human; insulin; diabetes; post-prandial glucose level;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
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Pred. No. 3.7e-14;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NTATXATQRLXNFLXXXXXNXGPXLPXTXVGSNTY 37
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Location/Qualifiers 2. .7
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                                                                                                                                                                                      Ruby C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY22447 standard; peptide; 37 AA
                                                                                                                                                                                                                                                         Disclosure; Page; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               84.9%;
                            label= H18R
                                                                 /label= S28P
                                                                                                                             98WO-US000288
                                                                                                                                               98WO-US000288
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                                                                                                                                                                                      L'italian J, Musunuri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                  (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                         WPI; 1999-458254/38
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Misc-difference 18
                    Misc-difference
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                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 AA;
         sulfide-bond
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specification
                                                                                                                             09-JAN-1998;
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                                                                                     WO9934822-A1
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and sequence represents a number of any line and source as a many and account the invention relates to a liquid pharmaceutical formulation (A), that contains (wt./vol.): 0.01-0.5$ amylin agonist (I); 1-10$ carbohydrate or polyol (II); and 0.02-0.5$ accetate, phosphate, citrate or glutamate buffer (III); and has pH 3-6. (A) are used, in conjunction with insulin, for treatment of diabetes, specifically to reduce post-prandial increases in glucose levels of the blood. In these formulations, (I) is stabilised, especially against deamidation and peptide bond hydrolysis for up to 4 years at 5 degrees C and 30 days at 30 degrees C, without addition of a separate stabiliser. They also retain short-term (up to 24 har) stability when combined with insulih, allowing both agents to be administered together, reducing the number of injections required. Note: This sequence was created by the indexer from information given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stabilized liquid formulation for treatment of insulin-dependent diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents a human amylin analogue, that acts as a amylin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human amylin agonist peptide 18-Arg25,28-Pro-amylin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruby
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label= F23L
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Best Local Similarity
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37 AA;
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(AMYL-) AMYLIN PHARM INC.
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                                                                                                                                                                                                                                               This invention relates to a method for treating or preventing gastritis or gastric ulceration which comprises administering amylin or an amylin agonist. Amylin administration is not carried out intra-cerebroventricularly. The specification describes a method for treating or preventing a condition for which a non-steroidal anti-inflammatory agent (NSAID) is indicated, comprising administering amylin or amylin agonist, which is not calcitonin, together with NSAID and also a composition composition amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat humans by administering it subcutaneously, intravenously or by nasal, oral, pulmonary, transdermal and buccal routes. The method is and other condition where an NSAID would be indicated. The present sequence is an example of an agonist used in the method
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                                                                                                                                   Beynon GW
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Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                          (AMYL-) AMYLIN PHARM INC.
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This invention relates to a method for treating or preventing gastritis or gastric ulceration which comprises administering amylin or an amylin agonist. Amylin administration is not carried out intraccerebroventricularly. The specification describes a method for treating or preventing a condition for which a non-steroidal anti-inflammatory agent (NSAID) is indicated, comprising administering amylin or amylin agonist, which is not calcitonin, together with NSAID and also a composition comprising an amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat humans by administering it subcutaneously, intravenously or by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat pain, fever, inflammation, arthritis, hypercoagulation sequence is an example of an agonist used in the method
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Beynon GW;
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                                This invention relates to a method for treating or preventing gastritis or gastric ulceration which comprises administering amylin or an amylin agonist. Amylin administration is not carried out intracerebroventricularly. The specification describes a method for treating or preventing a condition for which a non-steroidal anti-inflammatory agent (NSAID) is indicated, comprising administering amylin or amylin agonist, which is not calcitonin, together with NSAID and also a composition comprising an amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is used to treat humans by administering it subcutaneously, intravenously or by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat pain, fever, inflammation, arthritis, hypercoagulation and other condition where an NSAID would be indicated. The present sequence is an example of an agonist used in the method
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68.6%; Pred. No. 3.7e-14;
iive 0; Mismatches 11;
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nes 24; Conservative
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agent (NSAID) is indicated, comprising administering amylin or amylin agonist, which is not calcitonin, together with NSAID and also a composition comprising an amylin or an amylin agonist or their salts, except calcitonin and a NSAID in a carrier. The amylin composition is used to treat humans by administering it subcutaneously, intravenously or by nasal, oral, pulmonary, transdermal and buccal routes. The method is also used to treat pain, fever, inflammation, arthritis, hypercoagulation and other condition where an NSAID would be indicated. The present sequence is an example of an agonist used in the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
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68.6%; Pred. No. 3.7e-14;
tive 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-2000.
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Gaps

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Indele

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Mismatches

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Conservative
                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                15-JAN-2001
                                                                                                                                                                                                                                                                                                                                     US6114304-A
                                                                                                                                                                                                                                                                                                                                                            05-SEP-2000
24;
                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young AA,
                                                                                                                           AAB18574;
 Matches
                                                                               RESULT 42
                                                                                           AAB18574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an amylin agonist analogue compound. Amylin or amylin agonists are administered for reducing gastric motility or delaying gastric emptying, and for treating postprandial dumping syndrome or postprandial hyperslycemia, by inducing amylin activity, in a mammal. The peptides are used to reduce gastric motility or for delaying gastric emptying in a mammal undergoing gastrointestinal diagnostic procedures, such as radiological examination or magnetic resonance imaging. They are also used for reducing gastric motility in gastrointestinal disorder, especially spasm, which is associated with a disorder of acute diverticulities or disorders of biliary tract or sphincter of oddi. They are also used to treat postprandial dumping syndrome or postprandial hyperglycemia
                                                                                                                                                                                                                                                                             Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycentia; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating gastrointestinal disorder e.g. spasm by reducing gastric motility or delaying gastric emptying, postprandial dumping syndrome or postprandial hyperglycemia, by administering amylin or amylin agonist.
                                                                                Gaps
 to treat postprandial dumping
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                                                                                                                                                                                                                                                      Amino acid sequence of an amylin agonist analogue compound
                                                         Length 37;
                                                                                11; Indels
                                                       Score 118; DB 3;
Pred. No. 3.7e-14;
0; Mismatches 11;
                                                                                                     3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY 37
                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kolterman OG;
                                                                                                                          NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                               /note= "amidated residue"
 sphincter of oddi. They are also used t
syndrome or postprandial hyperglycemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 45-46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown KAK,
                                                                                                                                                                                    AAB18585 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00302069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00118381
                                                         84.9%;
                                                                                                                                                                                                                                 (first entry)
                                                                                24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-601336/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rink TJ,
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 AA;
                                  Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1993;
                                                                                                                                                                                                                                  15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    US6114304-A
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                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young AA,
                                                                                                                                                                                                          AAB18585
                                                        Query Match
Best Local
                                                                                                                                                                          AAB18585
ID AAB1
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Length 37;

Score 118; DB 3; Pred. No. 3.7e-14;

84.9%; 68.6%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amylin agonist, amylin, gastric motility, gastric emptying, postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating gastrointestinal disorder e.g. spasm by reducing gastric motility or delaying gastric emptying, postprandial dumping syndrome or postprandial hyperglycemia, by administering amylin or amylin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of an amylin agonist analogue compound.
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Pred. No. 3.7e-14;
0; Mismatches 11; Indels
37
                                                               37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kolterman OG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTATCATORLANFLVRSSNNLGPVLPSTNVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY
      3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 37-38; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                              AAB18574 standard; peptide; 37 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00302069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.68;
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMYL-) AMYLIN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-601336/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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Pred. No. 3.7e-14;

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Similarity
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Best Local S
Matches 25
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Best Local {
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                                                                                                                                                   RESULT 44
                                                                                                                                                                       AAB18583
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                                                                                                                                                                                                                                                                                                                                                             /note= "this residue, and residue 7, are independently selected residues having side chains which are chemically bonded to each other to form an intramolecular linkage comprising a disulphide bond, a lactam or a thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "this residue, and residue 2, are independently selected residues having side chains which are chemically bonded to each other to form an intramolecular linkage comprising a disulphide bond, a lactam or a thioester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an amylin agonist analogue compound. Amylin or amylin agonists are administered for reducing gastric motility or delaying gastric emptying, and for treating postprandial dumping syndrome or postprandial hyperglycemia, by inducing amylin activity, in amammal. The peptides are used to reduce gastric motility or for delaying gastric emptying in a mammal undergoing gastrointestinal diagnostic imaging. They are also used for reducing gastric motility in gastrointestinal disorder, especially spasm, which is associated with a disorder of acute diverticulities or disorders by biliary tract or sphincter of oddi. They are also used to treat postprandial dumping syndrome or postprandial hyperglycemia. note: the present sequence does not appear in the specification; it was created using information
                                                                                                                                                                                           Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal disgnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating gastrointestinal disorder e.g. spasm by reducing gastric motility or delaying gastric emptying, postprandial dumping syndrome opostprandial hyperglycemia, by administering amylin or amylin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "this residue is and alkylamino, dialkylamino, cycloalkylamino, arylamino, aryloxy, or aralkyloxy"
                                                                                                                                                       sequence of an amylin agonist analogue compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kolterman OG;
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                       AAB18604 standard; peptide; 37 AA
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                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rink TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37 AA;
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                                                                                                                 15-JAN-2001
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                                                                                                                                                                                                                                                                                         Synthetic
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                                                                             AAB18604;
     RESULT 43
AAB18604
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Length 37;

84.9%; Score 118; DB 3;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amylin agonist; amylin; gastric motility; gastric emptying; postprandial dumping syndrome; postprandial hyperglycemia; gastrointestinal diagnostic procedure; gastrointestinal disorder; spasm; acute diverticulitis; biliary tract disorder; sphincter of oddi disorder.
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                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of an amylin agonist analogue compound
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                        Indels
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68.6%; Pred. No. 3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown KAK, Kolterman OG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NTATXATORLANFLVHSNNNLGPVLPSTNVGSNTY
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                                                                          3 NTATXATORLXNFLXXXXXNXGPXLPXTXVGSNTY
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                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 43-44; 50pp; English.
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                                                                                                                                                                                                                                                                    AAB18583 standard; peptide; 37
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llarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMYL-) AMYLIN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young AA, Rink TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-601336/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Human amylin agonist 18Arg25,28Pro-h-amylin.

(first entry)

19-APR-2002

ABB05490;

ABB05490 standard; peptide; 37 AA

RESULT 46 ABB05490

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The present invention describes a liquid pharmaceutical formulation (A) comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or glutamate buffer (0.02 - 0.5) having a pH of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comprises a borosilicate glass vial having an open end, a stopper for multiuse compatible with the amylin and/or amylin agonist fixed in the open end of the vial. The package also comprises a cartridge for use in a pen injector. (A) has antidiabete; artivity and cartridge for use in a pen injector. (A) has antidiabete; The Commitation comprises amylin agonist which is biologically active, has a cartridge for use in a pen injector to precipitate in the presence of formulation comprises amylin agonist which is biologically active, has a reduced tendency to precipitate in the presence of compared to human amylin. The formulation maintains stability upon storage under refrigerated or room-temperature conditions. The compared to human amylin peptide analogue, which can be used as an or represents a human amylin peptide analogue, which can be used as an or amylin agonist in the present invention. With from the 37 amino acid human amylin as stated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbohydrate or polyhydric alcohol and
                                                                                                                                                                                                                                                                                                                                                                                   Human, amylin agonist, amylin peptide analogue, acetate, carbohydrate, liquid pharmaceutical formulation, polyhydric alcohol, phosphate, citrate, glutamate, buffer, antidiabetic, type II diabetes.
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68.6%; Pred. No. 3.7e-14;
iive 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                           Human amylin agonist 25Pro26Val28Pro-h-amylin.
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                                                                           ABB05496 standard; peptide; 37 AA.
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                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                       ABB05496;
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RESULT 45
                                           ABB05496
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The present invention describes a liquid pharmaceutical formulation (A) comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or glutamate buffer (0.02 - 0.5) having a pH of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comprises a borosilicate glass vial having an open end, a stopper for multiuse compatible with the amylin and/or amylin agonist cfixed in the open end of the vial. The package also comprises a corrulation comprises anylin agonist which is biologically activity and carbe used in the treatment of patients with type II diabetes. The formulation comprises amylin agonist which is biologically active, has a reduced tendency to form aggregates in water or at a presence of formulation comprises amylin. The formulation maintains stability upon storage under refrigerated or room-temperature conditions. The compared to human amylin, The formulation maintains stability upon storage under refrigerated or room-temperature conditions. The compared to human amylin postide analogue, which can be used as an or represents a human amylin peptide analogue, which can be used as an or amylin agonist in the present invention. Nab. The present sequence is not given in the present specification but is derived from the 37 amino acid human amylin as stated in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbohydrate or polyhydric alcohol and
                                                                                                                   Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate;
liquid pharmaceutical formulation; polyhydric alcohol; phosphate;
citrate; glutamate; buffer; antidiabetic; type II diabetes.
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Pred. No. 3.7e-14;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruby
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                                                                                                                                                                                                                                                                                                                        98US-00005262.
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Best Local Similarity
Matches 24; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-163554/21.
                                                                                                                                                                                                                                                                                                                                                                                           L'ITALIEN J
MUSUNURI S.
                                                                                                                                                                                                                                                    US2001043934-A1.
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                                                                                                                                                                                                                                                                                                                        09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (RUBY/) RUBY
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           08-JAN-1997;
                                                                                                                                                                                                                                                                                      22-NOV-2001
                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a buffer.
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Gaps

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3 NTATXATORLXNFLXXXXXXXXGPXLPXTXVGSNTY 37 NTATCATORLANFLVHSSNNFGPVLPSTNVGSNTY 37

Local Similarity 68.6 nes 24; Conservative

Best Loc Matches

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Query Match

Length 37; 11; Indels

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comperising (wt/vols) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or comperising (wt/vols) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or compercial package containing the liquid pharmaceutical formulation (A). The package compraises a borosilicate glass vial having an open end, a stopper for multiuse compatible with the amylin and/or amylin agonist (fixed in the open end of the vial and an aluminium band to retain the compering and of the vial. The package also comprises a carridge for use in a pen injector. (A) has antidiabetic activity and cartridge for use in a pen injector. (A) has antidiabetic activity and cornulation comprises amylin agonist which is biologically active, has a reduced tendency to formist with type II diabetes. The formulation comprises amylin agonist which is biologically active, has a reduced tendency to precipitate in the presence of than 2 psi and has a reduced tendency to precipitate in the presence of storage under refigerated or room-temperature conditions. The storage under refingerated or room-temperature conditions. The compared to human amylin, the formulation maintains seability upon compared to refigerate the vial of insulin in use. The present sequence of contributes in improved stability of the hormone and the patients no longer centles in improved stability of the hormone and the patients no longer centles in the present invention. N. B. The present sequence is not amylin agonist in the present invention and the patient specification but is derived from the 37 amino acid human amylin as stated in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbohydrate or polyhydric alcohol and
                                                                                                                                                                                                                                                                               Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate;
liquid pharmaceutical formulation; polyhydric alcohol; phosphate;
citrate; glutamate; buffer; antidiabetic; type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a liquid pharmaceutical formulation (A)
                                                                                                                                                                                                                                           Human amylin agonist 23Leu25Pro26Val28Pro-h-amylin.
3 NTATCATQRLANFLVRSSNNFGPILPSTNVGSNTY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             꾟
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 19pp; English.
                                                                                                         ABB05498 standard; peptide; 37
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                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LITA/) L'ITALIEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-163554/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MUSU/) MUSUNURI S.
(RUBY/) RUBY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                           US2001043934-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                      ABB05498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a buffer
                                                                  RESULT 47
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The present invention describes a liquid pharmaceutical formulation (A) comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or polyhydric alcohol (1 - 10) and an acetate, phosphate, citrate or glutamate buffer (0.02 - 0.5) having a pH of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comprises a borosilicate glass vial having an open end, a stopper for multiuse comparible with the amylin and/or amylin agonist fixed in the open end of the vial. The package also comprises a stopper in the far end of the vial. The package also comprises a catrity and can be used in the treatment of patients with type II diabetes. The commatrion comprises amylin agonist which is biologically active, has a reduced tendency to form aggregates in water or at a pressure of greater than 2 psi and has a reduced tendency to precipitate in the presence of the natural and has a reduced tendency to precipitate in the presence of storage under refrigerated or room-temperature conditions. The cormulation retains short-term mixing compatibility with insulin and results in improved stability of the hormone and the patients no longer represents a human amylin peptide analogue, which can be used as an creates and man amylin peptide analogue, which can be used as an or amylin agonist in the present invention. No. The present sequence is not given in the present specification but is derived from the 37 amino acid human amylin as stated in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbóhydrate or polyhydric alcohol and a buffer.
                                                                                                                                                                                                                                                                                     Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate; liquid pharmaceutical formulation; polyhydric alcohol; phosphate; citrate; glutamate; buffer; antidiabetic; type II diabetes.
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                                                                                                                                                                                                                                                 Human amylin agonist 18Arg23Leu25Pro26Val28Pro-h-amylin.
3 NTATCATQRLANFLVHSSNNLGPVLPSTNVGSNTY 37
                                                                                                                          ABB05500 standard; peptide; 37 AA
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Matches 24; Conservative
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MUSUNURI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-163554/21.
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
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                                                                                      RESULT 48
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Gaps .;

Length 37;

Score 118; DB 5; Length 37 Pred. No. 3.7e-14; 0; Mismatches 11; Indels

84.9%;

Ouery Match Best Local Similarity 68.6' Matches 24; Conservative

3 NTATXATQRLXNFLXXXXXXXXXGPXLPXTXVGSNTY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbohydrate or polyhydric alcohol and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a human amylin peptide analogue, which can be used as an amylin agonist in the present invention. N.B. The present sequence is not given in the present specification but is derived from the 37 amino acid human amylin as stated in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate;
liquid pharmaceutical formulation; polyhydric alcohol; phosphate;
citrate; glutamate; buffer; antidiabetic; type II diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human amylin agonist 18Arg23Leu25,28Pro-h-amylin.
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                                                                     37
                                        NTATXATORLXNFLXXXXXXXXCPXLPXTXVGSNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruby K;
                                                                                                                                                                                                                                                                         ABB05502 standard; peptide; 37 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MUSU/) MUSUNURI S.
(RUBY/) RUBY K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-1998;
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                                                                                                                                                                                           RESULT 49
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The present invention describes a liquid pharmaceutical formulation (A) comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a comprising (wt/vol*) an amylin agonist (0.01 - 0.5), a carbohydrate or a polyhydric alcohol (1 - 10) and an acetate, phosphate, cirrate or glutamate buffer (0.02 - 0.5) having a pH of 3 - 6. Also described is a commercial package containing the liquid pharmaceutical formulation (A). The package comparises a borosilicate glass vial having an open end, a stopper for multiuse compatible with the amylin and/or amylin agonist (fixed in the open end of the vial. The package also comprises a correcting for use in a pen injector. (A) has antidiabetic activity and carbe used in the treatment of patients with type II diabetes. The corrulation comprises amylin agonist which is biologically active, has a commulation comprises amylin agonist which is biologically active, has a commerced tendency to form aggregates in water or at a pressure of greater than 2 psi and has a reduced tendency to precipitate in the presence of than 2 psi and has a reduced tendency to precipitate in the presence of storage under refrigerated or room-temperature conditions. The compared to human amylin, The formulation maintains stability upon storage under refrigerate the vial of insulin in use. The present sequence is not represents a human amylin peptide analogue, which can be used as an or amylin agonist in the present invention. Whe present sequence is not given in the present specification but is derived from the 37 amino acid human amylin as stated in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pharmaceutical formulation useful for treating patients with type II diabetes comprises amylin agonist, carbohydrate or polyhydric alcohol and
                                                                                                                                                                                                                                                             Human; amylin agonist; amylin peptide analogue; acetate; carbohydrate;
liquid pharmaceutical formulation; polyhydric alcohol; phosphate;
citrate; glutamate; buffer; antidiabetic; type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 118; DB 5; Length 37;
Pred. No. 3.7e-14;
3 NTATCATORLANFLVRSSNNLGPILPSTNVGSNTY 37
                                                                                                                                                                                                                           Human amylin agonist 18Arg25,28Pro-h-amylin.
                                                                                                        ABB05487 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page; 19pp; English.
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68.6%;
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MUSUNURI S.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RUBY/) RUBY K.
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Synthetic.
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